

86691

Delaval, Jan

From: Gambel, Phillip
Sent: Thursday, February 13, 2003 9:52 AM
To: Delaval, Jan
Subject: 09 / 425516 freeman amd

jan

please perform a sequence and a sequence interference search for

ussn 09 / 425,516 (freeman amd)

SEQ ID NO: 2

SEQ ID NO: 23

thanx

phillip gambel
art unit 1644
308-3997

Room 8 Bx3

1644 mailbox 9e12

if by chance, you have done this recently,
please print out

this case was removed from my office and i don't see an updated sequence in the case

thanx

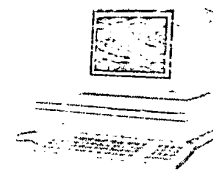
Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

08/152212

BioTech-Chem Library

Search Results

Feedback Form (Optional)



Scientific & Technical Information Center

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 308-4258
CM-1 Room 1E01

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* (Example: 1610)

➤ *Relevant prior art **found**, search results used as follows:*

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art **not found**:*

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Search results were not useful in determining patentability or understanding the invention.

Other Comments:

Drop off completed forms at the **Circulation Desk CM-1**, or send to Mary Hale, **CM1-1E01** or e-mail **mary.hale@uspto.gov**.

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OM protein - protein search, using sw model

Run on: February 13, 2003, 11:29:24 ; Search time 15.4702 Seconds
(without alignments)
2044.459 Million cell updates/sec

Title: US-09-425-516-2

Perfect score: 1733
Sequence: 1 MDPOQTWGLSNILFVMAFL.....AQRVFKSKTSCKSDTCF 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1733	100.0	329	1 A48754	B7-2 antigen - hum
2	1384	79.9	275	2 JC7604	CD86 spliced varia
3	963.5	55.6	330	2 I46691	CD86 precursor - r
4	743.5	42.9	309	2 I49522	gene B7-2 protein
5	522	30.1	110	2 JC7605	CD86 spliced varia
6	243	14.0	299	2 I46690	CD86 precursor - r
7	243	14.0	309	2 I49503	B-lymphocyte activ
8	222	12.8	321	2 I54766	B-lymphocyte activ
9	201.5	11.6	288	2 A45803	B-cell-restricted
10	187.5	10.8	289	2 G00031	B7 protein - red-c
11	173.5	10.0	487	2 S65133	butyrophilin - mou
12	167	9.6	526	2 S70587	butyrophilin - precu
13	162	9.3	526	2 A37821	butyrophilin - bov
14	136	7.8	365	2 JC7780	coxackie- and ade
15	131.5	7.6	1880	2 T18531	tractin - medicina
16	129.5	7.5	238	2 A49633	Ig lambda-like cha
17	128	7.4	274	2 A47639	OX-2 membrane glyco
18	128	7.4	278	1 TDRTOX	OX-2 membrane glyco
19	124	7.2	569	2 A46462	T cell activation
20	119.5	6.9	646	2 I38049	cell surface glyco
21	118.5	6.8	391	2 T09058	butyrophilin homol
22	113	6.5	1021	2 J19207	leukocyte surface
23	112.5	6.5	549	2 S04845	Ig heavy chain pre
24	110.5	6.4	994	2 I49276	c-mer tyrosine kin
25	109.5	6.3	230	2 S33161	Ig kappa chain - s
26	108.5	6.3	344	2 I56551	neurotrophin - rat
27	106	6.1	243	2 A53244	leukocyte antigen
28	105	6.1	335	2 S58892	signaling lymphocy
29	104.5	6.0	5175	2 T20992	hypothetical prote

30	104.5	6.0	5198	2	T43290	hemictentin precurs
31	104	6.0	292	2	T44230	hypothetical prote
32	103	5.9	871	1	I48696	protein-tyrosine k
33	103	5.9	881	1	I48697	protein-tyrosine k
34	102.5	5.9	391	2	G87723	protein R06A10.4 f
35	102	5.9	931	2	T39143	hypothetical prote
36	101.5	5.9	739	2	S18642	polynucleotide ade
37	101.5	5.9	784	2	T18452	hypothetical prote
38	101	5.8	167	2	T19084	hypothetical prote
39	101	5.8	1274	2	I40813	neurotoxin type F
40	100.5	5.8	416	2	A54017	colon carcinoma-as
41	99	5.7	570	2	A57535	intrleukin 1 recep
42	98.5	5.7	941	1	TVMVMD	protein-tyrosine k
43	98	5.7	588	2	A45254	surface glycoprote
44	98	5.7	664	2	T50316	hypothetical Armad
45	97.5	5.6	285	2	S36903	FC gamma (IG) rec

ALIGNMENTS

RESULT 1

A48754
B7-2 antigen - human
N:Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48754; S39055
R:Freeman, G.J.; Gribben, J.G.; Boussiotis, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombard, Science 262, 909-911, 1993
A:Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell prolif
A:Reference number: A48754; MUID:94053735; PMID:7694363
A:Accession: A48754
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-329 <PRE>
A:Cross-references: GB:I25259; NID:9416368; PIDN:AAAS8389.1; PID:9416369
N:Note: it is uncertain whether Met-1 or Met-7 is the initiator
R:Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somoza, C. Nature 366, 76-79, 1993
A:Title: B70 antigen is a second ligand for CTLA-4 and CD28.
A:Reference number: S39055; MUID:94050123; PMID:7694153
A:Accession: S39055
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 7-329 <AZU>
A:Cross-references: GB:U04343; NID:g439838; PIDN:AAB03814.1; PID:g439839
C:Genetics:
A:Gene: GDB:CD86; CD28LG2
A:Cross-references: GDB:433597; OMIM:601020
A:Map position: 3q13.3-3q21
C:Superfamily: B7-2 antigen
C:Keywords: glycoprotein

Query Match		100.0%;	Score 1733;	DB 1;	Length 329;
Best Local Similarity		100.0%;	Pred. No. 4e-121;		
Matches 329;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MDPOQTWGLSNILFVMAFLSQAAPLKIQAYFNETADLPQCFANSONQSLSELVVFWDQD	60		
DB	1	MDPOQTWGLSNILFVMAFLSQAAPLKIQAYFNETADLPQCFANSONQSLSELVVFWDQD	60		
QY	61	ENLVNLEVLGKGFDSVHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM	120		
DB	61	ENLVNLEVLGKGFDSVHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM	120		
QY	121	IRIHMNSLSVLANSQEPPIPIINITENYINLTCSHIGYPEPKMVKVLLRTKNSTI	180		
DB	121	IRIHMNSLSVLANSQEPPIPIINITENYINLTCSHIGYPEPKMVKVLLRTKNSTI	180		
QY	181	EYDGMQKSDNVNTELYDVSIISVSFPDVTNNMTIFCILETDKTLLSPFSIELEDPQ	240		
DB	181	EYDGMQKSDNVNTELYDVSIISVSFPDVTNNMTIFCILETDKTLLSPFSIELEDPQ	240		

Qy 241 PPDPHIPWITAVLPTVIICVMVFLILWKWKKKRPRNSYKCGTNTMEREESEQTKKREK 300
Db 241 PPDPHIPWITAVLPTVIICVMVFLILWKWKKKRPRNSYKCGTNTMEREESEQTKKREK 300
Qy 301 IHIPERSDEAQRVFKSKTSCKDSKDTCF 329
Db 301 IHIPERSDEAQRVFKSKTSCKDSKDTCF 329
RESULT 2
JC7604
CD86 spliced variant CD86 deltaTM isoform - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7604
R:Magistralli, G.; Caron, G.; Gauchat, J.F.; Jeannin, P.; Bonnefoy, J.Y.; Delneste, Y.
Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
A:Title: Identification of an alternatively spliced variant of human CD86 mRNA.
A:Reference number: JC7604; MUID:21092744; PMID:11162656
A:Accession: JC7604
A:Molecule type: mRNA
A:Residues: 1-275 <MAG>
C:Comment: This CD86 variant expressed by activated human monocytes, is a costimulatory
C:Gene: cd86deltaTM
C:Keywords: immune response
Query Match 79.9%; Score 1384; DB 2; Length 275;
Best Local Similarity 85.1%; Pred. No. 2.4e-95;
Matches 275; Conservative 0; Mismatches 0; Indels 48; Gaps 1;
Qy 7 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQFANSONQSLSELVVFWDQOENLVN 66
Db 1 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQFANSONQSLSELVVFWDQOENLVN 60
Qy 67 EYVLGKEKEDSVHSKYMGRTSFDSDSWTLRLHNLQIKDGLGYOCIIHHKKPTGMIRHOM 126
Db 61 EYVLGKEKEDSVHSKYMGRTSFDSDSWTLRLHNLQIKDGLGYOCIIHHKKPTGMIRHOM 120
Qy 127 NSELVLANFSPQEIPIVPSINITENVYINLTCSIIHGYPPEPKMSVLLRTKNSIYDGM 186
Db 121 NSELVLANFSPQEIPIVPSINITENVYINLTCSIIHGYPPEPKMSVLLRTKNSIYDGM 180
Qy 187 QKSDNVTELYDVSISLSVSPDVTNNMTIFCILETDKTRLLSSPFSIELEDQPPPDHI 246
Db 181 QKSDNVTELYDVSISLSVSPDVTNNMTIFCILETDKTRLLSSPFSI----- 228
Qy 247 PWITAVLPTVIICVMVFLILWKWKKKRPRNSYKCGTNTMEREESEQTKKREKIHIPER 306
Db 229 -----GNTWREBESEQTKKREKIHIPER 252
Qy 307 SDEAQRVFKSKTSCKDSKDTCF 329
Db 253 SDEAQRVFKSKTSCKDSKDTCF 275
RESULT 3
I46691
CD86 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 23-Jul-1999
C:Accession: I46691
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule
A:Reference number: I46689; MUID:95369849; PMID:7642234
A:Accession: I46691
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-330 <ISO>
A:Cross-references: GB:D49842; NID:g755098; PIDN:BAA08642.1; PID:g755099
C:Superfamily: B7-2 antigen

Query Match 55.6%; Score 963.5; DB 2; Length 330;
Best Local Similarity 58.0%; Pred. No. 4.5e-64;
Matches 192; Conservative 52; Mismatches 84; Indels 3; Gaps 3;
Qy 1 MDPOCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQFANSONQSLSELVVFWDQD 60
Db 1 MDAGCTMGLSVTVFVMAFLLSGAASLRIQAYFNKTADLPQCFNTSQSRSLSELVVFWDQD 60
Qy 61 ENLVINEVYLGEKEDSVHSKYMGRTSFDSDSWTLRLHNLQIKDGLGYOCIIHHKKPTGM 120
Db 61 ERLVLYELFLGREKPDNDVPKYIGTSFDOESWNLQLHNVOIKDKGVYQCFVHRGAKGL 120
Qy 121 IRIHOMNSELVLANFSPQEIPIVPSINITENVYINLTCSIIHGYPPEPKMSVLLRTKNSI 180
Db 121 VPIQNMNSELVLANFSPQEIPIVPSINITENVYINLTCSIIHGYPPEPKMSVLLRTKNSI 180
Qy 181 EYDGMQSDNVTELYDVSISLSVSPDVTNNMTIFCILETDKTRLLSSPFSIELEDQD 240
Db 181 EYDGVIEKSDNVTELYDVSISLSVSPDVTNNMTIFCILETDKTRLLSSPFSIELEDQD 240
Qy 241 PPPDHPITAV-LPTVIICVMVFLILWKWKKKRPRNSYKCGTNTMEREESEQTKKRE 299
Db 241 PVKEPRLWIAAVALTLIVVCGIVLFLTLWKRKKEQP-GVCECETIKMDKAENHVEERV 299
Qy 300 KIHIPER-SDEAQRVFKSKTSCKDSKDTCF 329
Db 300 KIHEPEKIPAKAAKCEHRLKTFSSDKSAHF 330
RESULT 4
I49522
gene B7-2 protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I49522
R:Freeman, G.J.; Borriello, F.; Hodes, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim, J. Exp. Med. 178, 2185-2192, 1993
A:Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell pro
A:Reference number: I49522; MUID:94065585; PMID:7504059
A:Accession: I49522
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-309 <RES>
A:Cross-references: GB:L25606; NID:g432478; PIDN:AAA9770.1; PID:g432479
C:Genetics
A:Gene: B7-2
C:Superfamily: B7-2 antigen
Query Match 42.9%; Score 743.5; DB 2; Length 309;
Best Local Similarity 51.5%; Pred. No. 8.4e-48;
Matches 159; Conservative 45; Mismatches 91; Indels 13; Gaps 5;
Qy 1 MDPOCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQFANSONQSLSELVVFWDQD 60
Db 1 MDPRCTMGLAILFVTVLLISDAVSVEYQAYFNGTAYLPCPFTKAQNSLSELVVFWDQD 60
Qy 61 ENLVINEVYLGEKEDSVHSKYMGRTSFDSDSWTLRLHNLQIKDGLGYOCIIHHKKPTGM 120
Db 61 QKLVLYEHVLTGTEKLDVNAKYLGRTSFDRNNTLRLHNLQIKDGMGYDQCFIQKPTGS 120
Qy 121 IRIHOMNSELVLANFSPQEIPIVPSINITENVYINLTCSIIHGYPPEPKMSVLLRTKNSI 180
Db 121 ILQQTLETSLVIANFSPQEIPIVPSINITENVYINLTCSIIHGYPPEPKMSVLLRTKNSI 178
Qy 181 EYDGMQSDNVTELYDVSISLSVSPDVTNNMTIFCILETDKTRLLSSPFSIELEDQD 240
Db 179 EYGDNQISODNVTELYDVSISLSVSPDVTNNMTIFCILETDKTRLLSSPFSIELEDQD 238
Qy 241 PPPDHPITAV-LPTVIICVMVFLILWKWKKKRPRNSYKCGTNTMEREESEQTKK 298
Db 239 P---QTVWEITASVTALLVLM--LIIVCHKKPNQPSRP----SNTASKLERDSNADR 289

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QY 299 EKIHPE 305
Db 290 ETINKE 296

RESULT 5
JC7605
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7605
R:Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeannin, P.; Bonnefoy, J.Y.; Delneste, Y.
Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
A:Title: Identification of an alternatively spliced variant of human CD86 mRNA.
A:Reference number: JC7604; MUID:21092744; PMID:11162656
A:Accession: JC7605
A:Molecule type: mRNA
A:Residues: 1-110 <MAG>
C:Comment: This CD86 variant expressed by nonstimulated human monocytes, as a membrane m
tion.
C:Genetics:
A:Gene: cd86deltaEC

Query Match 30.1%; Score 522; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.8e-32;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 ELEDPPPPHIPWITAVLPTVILICVMVFCLILWKWKKKRPNRSYKCGTNTMERSESEQ 294
Db 16 ELEDPPPPHIPWITAVLPTVILICVMVFCLILWKWKKKRPNRSYKCGTNTMERSESEQ 75

QY 295 TKREKIHIPERSDEAQRVFKSSKTSCKSDTCF 329
Db 76 TKREKIHIPERSDEAQRVFKSSKTSCKSDTCF 110

RESULT 6
I46690
CD80 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
C:Accession: I46690
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecu
A:Reference number: I46689; MUID:95369849; PMID:7642234
A:Accession: I46690
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-299 <ISO>
A:Cross-references: GB:D49843; NID:G755096; PIDN:BAA08643.1; PID:G755097
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 14.0%; Score 243; DB 2; Length 299;
Best Local Similarity 25.8%; Pred. No. 1e-10;
Matches 81; Conservative 65; Mismatches 122; Indels 46; Gaps 14;

QY 3 PQCTMGLSNILFVMAFLISGAAPLKIQAIFYNETADLPFCOFANSONQSLSLVVFWQDOENLVANEV 62
Db 12 PRCLHLKCLLLALAGLHFSSGISOVTKSVKEMAALSCDY-NISDELARMRIYWKDQQ 70

QY 63 LVLNEVYLKGFDSVHSKYMGRSFD-SDSWTLRLHNLQIKDGLYQCIIHHKKTGMIRI-HQWN 121
Db 71 MVLIS-IISQVE---VWPEYKNRTFPDIIINNLSLIMIALRLSDKGTTCVVKNGNSGFR 126

QY 122 RIHOMSELVLANSQPEIPIISNITENVYINLTCSHIGYPEPKMVL---RMSVLLRTKN 177
Db 127 REHLTSVTLISRADPVSITDIGHPPNVK-RIRCSAGGPFPEPLAWMEDGELNAVN 185

QY 178 STIEYDGMKQSDNVTELYDVSLVSFPDVTSNMTIFCILETDKTRLLSSPFSIELE 237
Db 186 TTVD-----QDLDTELYSSSELOF---NVTNNHSIVCLIKYGELS-VSQIFPWSPK 233
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```
QY 238 DRQPPPHIP-WITAVLPT-----VILICVMVFCLI---LWKWKKKRPNRSYKCGTNTMER 289
Db 234 KOEPPIDQLPFWV--IIPVSGALVLTAVVLYCLACRHVARWKTRR-----N 278

QY 290 EESEQTKKREKIHI 303
Db 279 EETVGTGTERLSPIYL 292

RESULT 7
I49503
B-lymphocyte activation antigen 7 precursor - mouse
N:Alternate names: MB7-2
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C:Accession: I49503; S17291; I49521
R:Selvakumar, A.; White, P.C.; Dupont, B.
Immunogenetics 38, 292-295, 1993
A:Title: Genomic organization of the murine B-lymphocyte activation antigen B7.
A:Reference number: I49503; MUID:93307789; PMID:7686531
A:Accession: I49503
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-309 <RES>
A:Cross-references: GB:L12589; NID:G293299; PIDN:AAA37240.1; PID:G293301
R:Freeman, G.J.; Gray, G.S.; Gimmi, C.D.; Lombard, D.B.; Zhou, L.J.; White, M.; Fingerot
J. Exp. Med. 174, 625-631, 1991
A:Title: Structure, expression, and T cell costimulatory activity of the murine homologi
A:Reference number: S17291; MUID:91341422; PMID:1714935
A:Accession: S17291
A:Molecule type: mRNA
A:Residues: 1-274, 'R', 279-309 <FRE>
A:Cross-references: EMBL:X60958; NID:G50111; PIDN:CAA43291.1; PID:G50112
R:Inobe, M.; Linsley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tanakoshi, M.; Uede, T.
Biochem. Biophys. Res. Commun. 200, 443-449, 1994
A:Title: Identification of an alternatively spliced form of the murine homologue of B7.
A:Reference number: I49521; MUID:94220123; PMID:7513163
A:Accession: I49521
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-143, 238-274, 'R', 279-309 <R2>
A:Cross-references: GB:D16220; NID:G5051118; PIDN:BAA03748.1; PID:G994769
C:Genetics:
A:Gene: B7
A:Introns: 37/1; 143/1; 237/1; 275/1
C:Superfamily: B-lymphocyte restricted antigen B7
C:Keywords: alternative splicing

Query Match 14.0%; Score 243; DB 2; Length 309;
Best Local Similarity 29.8%; Pred. No. 1.1e-10;
Matches 91; Conservative 53; Mismatches 119; Indels 42; Gaps 16;

QY 12 ILFVMAFLISGAAPLKIQAIFYNETAD---LPCOFANSONQSLSLVVFWQDOENLVANEV 68
Db 23 LLFVLLIRLSQVSDVDQLSKSKDKVLLPCRY-NSPHEDESEDRYKQHKDVLS-V 80

QY 69 YLGEKEDFSVHSKYMGRSFDSDSWTLRLHNLQIKDGLYQCIIHHKKTGMIRI-HQWN 127
Db 81 TAGKLK---VWPEYKNRTLYDNTYSLIILGLVLSDRGTGTCVW-OKKRGTYEVKHLAL 136

QY 128 SELSVLANFSQPEIPIISNITENVYINLTCSHIGYPEPKMVL-----LRTKNSTIEY 182
Db 137 VKLSIKADFSFENITSGNPSADTK-RITCFASGGFPKP-RFSWLENGRELPGINTTI-- 192

QY 183 DGMKQSDNVTELYDVSLVSFPDVTSNMTIFCILETDKTRLLSSPFSIELEDPQPP 242
Db 193 -----SQDPESELYTISOLOF---NITRNHTIKLKIYGDAAH-VSEDTWE-KPPEDP 241

QY 243 PDHIPWIT-----AVLPTVILICVMVFCLILWKWKKKRPNRSYKCGTN---TWERSE- 291
Db 242 PDSKNTLVLFAGAGGAVITWVIVIIKCFCKHNLQSCFRNEASRETNNSLITGPEEA 301

QY 292 -SEQT 295
```


C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002
C:Accession: JC7780
R:Thoenen, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.
Biochem. Biophys. Res. Commun. 288, 805-808, 2001
A:Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus receptor
A:Reference number: JC7780
A:Contents: Liver
A:Accession: JC7780
A:Molecule type: mRNA
A:Residues: 1-365 <PRO>
A:Cross-references: GB:AV033651
C:Comment: This protein serves as the primary adenoviral attachment site on bovine cells

Query Match 7.8%; Score 136; DB 2; Length 365;
Best Local Similarity 23.3%; Pred. No. 0.011;
Matches 86; Conservative 44; Mismatches 109; Indels 130; Gaps 20;

QY 13 LFWNAFLSGAAPL-----KIQAFNETADLPQF-----ANS 45

DB 3 LLRFLLLCGVADFTGSLITTPQMIKAKGETAYLPCKFTLGPEDQGLDIEWLLSPA 62

QY 46 QNQSLSLVVFWQDQENLVNEVLGKEFDSVHSKYMGRTSFSDSW-----TLRLHNL 100

DB 63 DNQKVDQVII-----LYSGDKIYDYYQDLKGRVHFTSNDLKGDSASINVTNL 110

QY 101 QIKDKGLYQCIHHKPTGMIRIHMNSLSVLANSFQPEIVPISNITENVYN----- 154

DB 111 QLSDIGTYQCKV--KKAPG---VGNKKIQTULV-----VKPSGI--RCYVDGSEIG 155

QY 155 ---LTCSSIHGYPEPKMSVLLRTKNSIETDYGIMQKSDQNVTELYDVSISLSVSF--PD 209

DB 156 NDFKJLKC-----EPKESLPLR-----YE--WQKLSL-----SQKLPTSWLPE 191

QY 210 VTSNM-----TIFCILETDKTRLLSPFSEIELEDPQPPDHIPMIT-----AV 252

DB 192 MTSFVTSVKNSAEVSGTYTC---TVNRVGSQCLRL--DVVPPSNRAGTIAGAVIGTL 247

QY 253 LPTVVICVMVFCLILMKWKKKRPNRSYKCGTNTMERSEBQTKKREKIHIPERSDEAQR 312

DB 248 LALVLIALIVFCC-----HKKREEKY-----EKEVHHDIREDVPPPKSTRTSTAR 292

QY 313 VFKSSKTSS 321

DB 293 SYIGSNHSS 301

RESULT 15

Tl8531

Tractin - medicinal leech

C:Species: Hirudo medicinalis (medicinal leech)

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-May-2000

C:Accession: Tl8531

R:Huang, Y.; Jellies, J.; Johansen, K.M.; Johansen, J.

J. Cell Biol. 138, 143-157, 1997

A:Title: Differential glycosylation of Tractin and LeechCAM, two novel Ig-superfamily members

A:Reference number: Z18951; MUID:97362067; PMID:9214388

A:Accession: Tl8531

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: mRNA

A:Residues: 1-1880 <HUA>

A:Cross-references: EMBL:U92813; NID:g2275259; PID:g2275260; PIDN:AAC47654.1

Query Match 7.6%; Score 131.5; DB 2; Length 1880;

Best Local Similarity 20.0%; Pred. No. 0.21;

Matches 87; Conservative 60; Mismatches 144; Indels 143; Gaps 19;

QY 1 MDPOCTMGLSNILFWNAFLISGAAPLKIQAYFN-----ETADLPQCF 42

DB 1 MNPQ---AMPPLQEQACFLLLATTTMTQKEVNRPPSITAHPPYSTFKNMEVEIFCEA 57

QY 43 ANSQNSLSLVVFW-QDQENLVNLNEVLGKEFDSVHSKYMGRTSFSDSWTLRLHNLQ 101

DB 58 TGT-----PPLVFWQFKDGEPLKSEA-----ERPFKDQDQGITLYNNE 97

QY 102 IKDKGLYQCIHHKXPTG-----MIRIHMNSLSVLANSFQPEIVPISNITENVYNLT 156

DB 98 LKDEGYQOCIVRNKNGYTAASVKTLLKMAVQESFPTV-----KEQIV---NVRVGDNLTLR 150

QY 157 CSSIHGYPEP-----KKMSVLLRTKNS---TIEYDG-----IMQKSDQNVTELYDVS 200

DB 151 CNPPKSYPTPDVYVGTVKKGAKLLPLENTMYNLDYEGNPHFANVME--EDHREGAYVLC 208

QY 201 ISLSVSF-PDVTSNMTIFCILETDKTRLLSSPFSIELEDPQ----- 241

DB 209 ISHNNAVRSSVQGNDCIIRINGSSKDGVRKHAPGVMMWTSRDKDLALTGOSKKLKCFSGY 268

QY 242 PPDHIPW-----ITAVLP-----TVIICVMVF 263

DB 269 PTPNVSKSRGSDFPKPIVVSSELPHLEIRNVEVGDAITYRCTGSSYTGKAVFVDIELT 328

QY 264 CLILWKWKKKRPRN-----SYKCGTNTMERSE--QTKKREKIHIPE---RSDE 309

DB 329 VESMPRWKDKRPEDVNTSDSETAVFKCGVEGIPRPTVEMWMLNKRPLEDLPNPRMRMD 388

QY 310 AQRVFKSSKTSSCD 323

DB 389 ERTVLTFNSVSSKD 402

Search completed: February 13, 2003, 11:33:20

Job time : 17.4702 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 11:23:59 ; Search time 17.5329 Seconds
(without alignments)
778.291 Million cell updates/sec

Title: US-09-425-516-2

Perfect score: 1733

Sequence: 1 MDPOQTWGLSNILFVMAFL.....AORVFKSSKTSCKSDKDTCF 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1733	100.0	329	1 CD86 HUMAN	P42081 homo sapien
2	963.5	55.6	330	1 CD86 RABIT	P42071 oryctolagus
3	743.5	42.9	309	1 CD86 MOUSE	P42082 mus musculus
4	244	14.1	306	1 CD80 MOUSE	Q00609 mus musculus
5	243	14.0	299	1 CD80 RABIT	P42070 oryctolagus
6	201.5	11.6	288	1 CD80 HUMAN	P33681 homo sapien
7	179	10.3	524	1 BUTY MOUSE	Q62556 mus musculus
8	175.5	10.1	322	1 ICOL MOUSE	Q9jh38 mus musculus
9	167	9.6	526	1 BUTY HUMAN	Q13410 homo sapien
10	165.5	9.5	302	1 ICOL HUMAN	Q75144 homo sapien
11	162	9.3	526	1 BUTY BOVIN	P18892 bos taurus
12	128	7.4	274	1 OK2G HUMAN	P41217 homo sapien
13	128	7.4	278	1 OK2G RAT	P04218 rattus norv
14	124.5	7.2	365	1 CXAR MOUSE	P97792 mus musculus
15	124	7.2	569	1 TACT HUMAN	P40200 homo sapien
16	119.5	6.9	646	1 MU18 HUMAN	P43121 homo sapien
17	118.5	6.8	365	1 CXAR HUMAN	P78310 homo sapien
18	114	6.6	837	1 NCM2 MOUSE	Q35136 mus musculus
19	110.5	6.4	994	1 MERK MOUSE	Q50805 mus musculus
20	109.5	6.3	994	1 MERK RAT	P70797 rattus norv
21	109	6.3	348	1 K1LO RAT	P92038 rattus norv
22	108.5	6.3	344	1 NTRI RAT	Q62718 rattus norv
23	106	6.1	243	1 CD48 HUMAN	P09326 homo sapien
24	105	6.1	335	1 SLAM HUMAN	Q13291 homo sapien
25	103.5	6.0	515	1 PVR1 MOUSE	Q9ikf6 mus musculus
26	102	5.9	484	1 PAP2 XENLA	P51005 xenopus lae
27	101.5	5.9	517	1 PVR HUMAN	Q15223 homo sapien
28	101.5	5.9	738	1 PAP BOVIN	P25500 bos taurus
29	101	5.8	1274	1 BKF CLOBO	P30996 clostridium
30	100.5	5.8	337	1 G55A CHICK	Q98892 gallus gall
31	99	5.7	564	1 C166 BRARE	Q90460 brachydanio
32	98.5	5.7	978	1 KPMS FSVMD	P00545 feline sarc
33	97.5	5.6	285	1 FCG2 RAT	Q63203 rattus norv

34	97.5	5.6	319	1 A33 HUMAN	Q99795 homo sapien
35	97.5	5.6	977	1 KPMS MOUSE	P09581 mus musculus
36	97.5	5.6	978	1 KPMS RAT	Q00495 rattus norv
37	97	5.6	298	1 JAM1 BOVIN	Q9xt56 bos taurus
38	97	5.6	315	1 HEMA VACCT	P16561 vaccinia vi
39	97	5.6	343	1 SLAM MOUSE	Q9qum4 mus musculus
40	96	5.5	246	1 MOG BOVIN	P55803 bos taurus
41	96	5.5	246	1 MOG MOUSE	Q61885 mus musculus
42	95	5.5	417	1 PVR HUMAN	P15151 homo sapien
43	94.5	5.5	583	1 C166 MOUSE	Q61490 mus musculus
44	94.5	5.5	588	1 C166 CHICK	P42292 gallus gall
45	94.5	5.5	873	1 FAS2 DROME	P34082 drosophila

ALIGNMENTS

RESULT 1
CD86_HUMAN
ID_CD86_HUMAN STANDARD; PRT; 329 AA.
AC P42081; Q13655;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T lymphocyte activation antigen CD86 precursor (Activation B7-2 antigen) (CTLA-4 counter-receptor B7.2) (B70) (FUN-1) (BU63).
GN CD86 OR CD28LG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=94053735; PubMed=7694363;
RA Freeman G.J., Gribben J.G., Boussiotis V.A., Ng J.W., Restivo V.A., Jr., Lombard L.A., Gray G.S., Nadler L.M.;
RT "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell proliferation.";
RL Science 262:909-911(1993).
RN [2]
RP SEQUENCE OF 7-329 FROM N.A.
RX MEDLINE=94050123; PubMed=7694153;
RA Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H., Lanier L.L., Somoza C.;
RT "B70 antigen is a second ligand for CTLA-4 and CD28.";
RL Nature 366:76-79(1993).
RN [3]
RP SEQUENCE OF 7-329 FROM N.A.
RX TISSUE=Foreakin;
RA Jellis C.L., Wang S.S., Rennett P., Borriello F., Sharpe A.H., Green N.R., Gray G.S.;
RT "Genomic organization of the gene coding for the costimulatory human B-lymphocyte antigen B7-2 (CD86).";
RL Immunogenetics 42:85-89(1995).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=95088403; PubMed=7527824;
RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S., Okumura K., Ito D., Azuma M.;
RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T cell proliferation, cytokine production, and generation of CTL.";
RL J. Immunol. 154:97-105(1995).
RN [5]
RP IDENTIFICATION AS CD86.
RX MEDLINE=94348060; PubMed=7520767;
RA Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M., Nadler L.M., Wakasa H., Tedder T.F.;
RT "The B7-2 (B70) costimulatory molecule expressed by monocytes and activated B lymphocytes is the CD86 differentiation antigen.";
RL Blood 84:1402-1407(1994).
CC -!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY

```
CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND
CC MONOCYTES.
CC
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD86 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd86.htm".
CC
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CC -----
CC EMBL; L25259; AAA58389.1; -.
CC EMBL; U04343; AAB03814.1; -.
CC EMBL; U17722; AAA86473.1; -.
CC EMBL; U17717; AAA86473.1; JOINED.
CC EMBL; U17718; AAA86473.1; JOINED.
CC EMBL; U17719; AAA86473.1; JOINED.
CC EMBL; U17721; AAA86473.1; JOINED.
CC Genew; HGNC:1705; CD86.
CC MIM; 601020; -.
CC InterPro; IPR003006; IG_MHC.
CC InterPro; IPR003596; IG_V.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00290; IG_MHC; FALSE NEG.
CC Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
CC Receptor.
CC SIGNAL 1 23 POTENTIAL.
CC CHAIN 24 329 T LYMPHOCYTE ACTIVATION ANTIGEN CD86.
CC DOMAIN 24 247 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 248 268 POTENTIAL.
CC DOMAIN 269 329 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 33 117 IG-LIKE V-TYPE DOMAIN.
CC DOMAIN 150 225 IG-LIKE C2-TYPE DOMAIN.
CC DISULFID 40 110 POTENTIAL.
CC DISULFID 157 218 POTENTIAL.
CC CARBOHYD 33 33 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 47 47 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 192 192 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 213 213 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CONFLICT 27 27 K -> E (IN REF. 3).
CC SEQUENCE 329 AA; 37696 MW; 65D4F3826889CF7D CRC64;
CC
CC Query Match 100.0%; Score 1733; DB 1; Length 329;
CC Best Local Similarity 100.0%; Pred No 1.4e-125;
CC Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 MDPQCTMGLSNILFWMAFLLSGAAPLKIQAIFNETADLPQCFANSONQSLSLVFWQDQ 60
CC DB 1 MDPQCTMGLSNILFWMAFLLSGAAPLKIQAIFNETADLPQCFANSONQSLSLVFWQDQ 60
CC
CC 61 ENLVNVLVYLGKEKEDSVHSYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKPTGM 120
CC DB 61 ENLVNVLVYLGKEKEDSVHSYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKPTGM 120
CC
CC 121 IRHONMSLSLVANFSPQEIPIVPSITNTENVIYINLTCSISIHGYPEPKMNSVLLRTKNSTI 180
CC DB 121 IRHONMSLSLVANFSPQEIPIVPSITNTENVIYINLTCSISIHGYPEPKMNSVLLRTKNSTI 180
CC
CC 181 EYDGIIMOKSDQNVNTELYDVSISSVSPDVTNSMTIFCILETDKTRLLSSPFSIELEDQ 240
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DB 181 EYDGIIMOKSDQNVNTELYDVSISSVSPDVTNSMTIFCILETDKTRLLSSPFSIELEDQ 240
QY 241 PPPHHIPIITAVLPTVIICWVFCILILWKWKKKRPRNSYKCGTNTMERSESEQTKKREK 300
DB 241 PPPHHIPIITAVLPTVIICWVFCILILWKWKKKRPRNSYKCGTNTMERSESEQTKKREK 300
QY 301 IHIPIERDEAQRVFKSSKTSKSSDCKSDTCF 329
DB 301 IHIPIERDEAQRVFKSSKTSKSSDCKSDTCF 329
CC
CC RESULT 2
CC CD86 RABIT STANDARD; PRT; 330 AA.
CC AC P42071;
CC DT 01-NOV-1995 (Rel. 32, Created)
CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, last annotation update)
CC DE B lymphocyte activation antigen CD86 precursor (Activation B7-2
CC antigen).
CC GN CD86.
CC OS Oryctolagus cuniculus (Rabbit).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CC OX NCBI_TaxID=9986;
CC RN [1]_
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=B/J X CHBB:HM;
CC RX MEDLINE=95369849; PubMed=7642234;
CC RA Isono T., Seto A.;
CC RT "Cloning and sequencing of the rabbit gene encoding T-cell
CC costimulatory molecules ";
CC RL Immunogenetics 42:217-220(1995).
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC
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CC -----
CC EMBL; D49842; BAA08642.1; -.
CC DR InterPro; IPR003006; IG_MHC.
CC DR InterPro; IPR003596; IG_V.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS00290; IG_MHC; 1.
CC KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
CC Receptor.
CC SIGNAL 1 22 POTENTIAL.
CC CHAIN 23 330 B LYMPHOCYTE ACTIVATION ANTIGEN CD86.
CC DOMAIN 23 247 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 248 268 POTENTIAL.
CC DOMAIN 269 330 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 33 117 IG-LIKE V-TYPE DOMAIN.
CC DOMAIN 150 225 IG-LIKE C2-TYPE DOMAIN.
CC DISULFID 40 110 POTENTIAL.
CC DISULFID 157 218 POTENTIAL.
CC CARBOHYD 33 33 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL) .
SQ SEQUENCE 330 AA; 37142 MW; 935CDD65C57E3EE1 CRC64;

Query Match 55.6%; Score 963.5; DB 1; Length 330;
Best Local Similarity 58.0%; Pred. No. 1.1e-66;
Matches 192; Conservative 52; Mismatches 84; Indels 3; Gaps 3;

QY 1 MDPOCTMGLSNILFVNAFLLSGAAPLKIQAYENETADLPQCFANSONQSLSELVVFWDQ 60
DB 1 MDACCTMGLSVTVFVWALLLSGAASLRQAYFNKTADLPQCFNQSOSLSSELVVFWDQ 60
QY 61 ENLVNLYLGKFKFDSVHSKYMGRTPSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
DB 61 ERLVLYELFGLREKPNVDPKYIGRTSPDQSMNLQHNQVQIKDKGVTCQFVHHRGAKGL 120
QY 121 IRIHOMNSELVLANFSQPEIPIGNITENVYINLTCSSTHGVPEPKMVSLLRTKSTI 180
DB 121 VPIYOMNSELVLANFTQPEITLISNITRNSAINLTCSVQGYPEPKMFFVLKTNATT 180
QY 181 EYDGMOKSDNTELYDVISLSVSPDVTNSNTIFCILETDKTRLLSSPFSIELEDPP 240
DB 181 EYDGVIEKSDNVTGLYNISISGTSFDDIRNATYCVLIQESTETYSQHFPPIVPADPV 240
QY 241 PPPDHIPMITAV-LPTVIICVMVFCLILWKWKKRPNSYKCGTNTWERESESQTKRE 299
DB 241 PVEPRLIWIAANVALTIIVCGVILFLLTWKKKEQOP-GVCECTIKMDKAENEHVSER 299
QY 300 KIHIPER-SDEAQRVFKSKTSSCDKSDTCF 329
DB 300 KIHPEKIPAKAAKCEHRLKTPSPDKSAAHF 330

RESULT 3
CD86_MOUSE STANDARD; PRT; 309 AA.
AC P42082;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T lymphocyte activation antigen CD86 precursor (Activation B7-2
DE antigen) (Early T cell costimulatory molecule-1) (ETC-1).
GN CD86.
OS Mus musculus (Mouse) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=94055585; PubMed=7504059;
RA Freeman G.J., Borriello F., Hodes R.J., Reiser H., Gribben J.G.,
RA Ng J.W., Kim J., Goldberg J.M., Hathcock K., Laszlo G., Lombard L.A.,
RA Wang S., Gray G.S., Nadler L.M., Sharpe A.H.;
RT "Murine B7-2, an alternative CTLA4 counter-receptor that costimulates
RT T cell proliferation and interleukin 2 production.";
RL J. Exp. Med. 178:2185-2192(1993).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=96094437; PubMed=7499829;
RA Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;
RT "Differential expression of alternate mB7-2 transcripts.";
RL J. Immunol. 155:5490-5497(1995).
RN [3]
RP SEQUENCE OF 7-309 FROM N.A.
RX MEDLINE=94230971; PubMed=7513726;
RA Chen C., Gault A., Shen L., Nabavi N.;
RT "Molecular cloning and expression of early T cell costimulatory
RT molecule-1 and its characterization as B7-2 molecule.";
RL J. Immunol. 152:4929-4936(1994).
CC -!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
```

```
CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION. BY
CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-7 IS THE INITIATOR.
CC
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CC
CC EMBL; L25606; AAA79770.1; -;
CC EMBL; U39456; AAC52334.1; -;
CC EMBL; U39459; AAC52334.1; JOINED.
CC EMBL; U39461; AAC52334.1; JOINED.
CC EMBL; U39462; AAC52334.1; JOINED.
CC EMBL; U39463; AAC52334.1; JOINED.
CC EMBL; U39464; AAC52334.1; JOINED.
CC EMBL; U39465; AAC52334.1; JOINED.
CC EMBL; U39466; AAC52334.1; JOINED.
CC EMBL; U39466; AAC52334.1; JOINED.
CC EMBL; U39466; AAC52336.1; ALT INIT.
CC EMBL; U39461; AAC52336.1; JOINED.
CC EMBL; U39462; AAC52336.1; JOINED.
CC EMBL; U39463; AAC52336.1; JOINED.
CC EMBL; U39464; AAC52336.1; JOINED.
CC EMBL; U39465; AAC52336.1; JOINED.
CC EMBL; U39466; AAC52336.1; JOINED.
CC EMBL; S70108; AAB30744.2; ALT_INIT.
CC MGD; MGI:101773; CD86.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV_1.
CC PROSITE; PS00290; IG_MHC; FALSE NEG.
CC Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
CC Receptor.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 309 T LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT DOMAIN 24 244 EXTRACELLULAR (POTENTIAL) .
FT TRANSMEM 245 265 POTENTIAL.
FT DOMAIN 266 309 CYTOPLASMIC (POTENTIAL) .
FT DOMAIN 33 117 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 150 223 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 40 110 POTENTIAL.
FT DISULFID 157 216 POTENTIAL.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL) .
SQ SEQUENCE 309 AA; 34665 MW; 8F58DCD1FB81D5EA CRC64;

Query Match 42.9%; Score 743.5; DB 1; Length 309;
Best Local Similarity 51.5%; Pred. No. 6.7e-50;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

QY 1 MDPOCTMGLSNILFVNAFLLSGAAPLKIQAYENETADLPQCFANSONQSLSELVVFWDQ 60
DB 1 MDPRCTMGLAILIFVTVLLISDAVSVEVQAVFNGTAYLPCTPFTKAQNISLSLVVFWDQ 60
QY 61 ENLVNLYLGKFKFDSVHSKYMGRTPSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
```

Db 61 QKLVLYEHLGTEKLDVNAKLGRTSPDRNNWTLRLHNVQIKDMGSDCFIQKPPG 120
QY 121 IRIHOMNSELVLANSFQEIPIVPSNITENVYINLTCSSIHGYPEPKMSVLLRKNSTI 180
Db 121 IILQOITELSVIANSEPEIKLAQNVTGNSGINLTCTSKQGHPPKQMYFLI--TNSTN 178
QY 181 EYDGMOKSDNVTLEYDVSISLVSFPDVTNNMTIFCILETDKTRLLSSPFSIELEDPQ 240
Db 179 EYGDNMQISODNVTFLFSISLSLSPDGVWHMTVVCLETESMKISSKPLNFTQFP 238
QY 241 PPPDHIPW--ITAVLPTVIICVMVFCILMLWKWKKKRPRNSYKCGTNTWEREESQTKR 298
Db 239 P--QTYWKEITASVTVALLLVML--LIIVCHKKPNQPSRP----SNTASKLERDSNADR 289
QY 299 EKIHIPE 305
Db 290 ETINLKE 296
RESULT 4
ID CD80 MOUSE STANDARD; PRT; 306 AA.
AC Q00609;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1 antigen) (B7).
GN CD80 OR B7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=91341422; PubMed=1714935;
RA Gray G.S., Freeman G.J., Gimmi C.D., Lombard D.B., Zhou L.J., White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;
RT "Structure, expression, and T cell costimulatory activity of the murine homologue of the human B lymphocyte activation antigen B7.";
RL J. Exp. Med. 174:625-631(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=93307789; PubMed=7686531;
RA Selvakumar A., White P.C., Dupont B.;
RT "Genomic organization of the mouse B-lymphocyte activation antigen B7.";
RL Immunogenetics 38:292-295(1993).
CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING B-CELL MALIGNANCIES.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
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CC -----CAA43291.1; -
DR EMBL; X60958; CAA43291.1; -
DR EMBL; L12589; AAA37240.1; ALT_SEQ.
DR EMBL; L12585; AAA37240.1; JOINED.
DR EMBL; L12586; AAA37240.1; JOINED.
DR EMBL; L12587; AAA37240.1; JOINED.
DR EMBL; L12588; AAA37240.1; JOINED.
DR PIR; S17291; S17291.
DR HSSP; P33681; 1DR9.
DR MGD; MGI.101775; Cd80.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; IG like; 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL 1 37
FT CHAIN 38 306
FT DOMAIN 38 246
FT TRANSMEM 247 268
FT DOMAIN 269 306
FT DOMAIN 47 126
FT DOMAIN 158 226
FT DOMAIN 227 246
FT DISULFID 54 119
FT DISULFID 165 219
FT CARBOHYD 93 93
FT CARBOHYD 99 99
FT CARBOHYD 149 149
FT CARBOHYD 189 189
FT CARBOHYD 210 210
FT CARBOHYD 214 214
SQ SEQUENCE 306 AA; 34589 MW; 1DBADE0931B84C62 CRC64;
Query Match 14.1%; Score 244; DB 1; Length 306;
Best Local Similarity 27.9%; Pred. No. 1.1e-11;
Matches 89; Conservative 58; Mismatches 120; Indels 52; Gaps 16;
QY 12 ILFWAFLLSGAAPLQIAYFNETAD---LPCQFANSQNSLSSELVFWQDOENLVLADEV 68
Db 23 LLFVLLRLSQVSDVDSEQLSKSVKDKVLLPCRY-NSPHEDESEDEIRYQKDKVLS-V 80
QY 69 YLGKEKFDVSVHXYMGRTSFDSDSWTLHLNLQIKDKGLYQCIIHHKKTGMIRI-HQMN 127
Db 81 TAGKLK--VMPEYKNRTLYDNTYSLIILGLVLSDRGTYSCVV-QKBERGTYEVKHLAL 136
QY 128 SELSVLANFSQPIVPSNITENVYINLTCSSIHGYPEPKMSVL-----LRTKNSTIEY 182
Db 137 VKLSIKADFTPTNITSGNPSADTK-RITCPASGGFPKP-RFSWLENGRELPGINTTII-- 192
QY 183 DGIWMQSQDNVTLEYDVSISLVSFPDVTNNMTIFCILETDKTRLLSSPFSIELEDPQPP 242
Db 193 -----SQDPESELYTIISSQLDF--NTRNHTIKCLIKYGDAAH-VSEDFTWE-KPPEDP 241
QY 243 PDHIPWIT-----AVLPTVIICVMVFCILMLWKWKKKRPRNSYKCGTNTWEREESQT 295
Db 242 PSDKNITVLFGAGFGAVITVVIVVILKFCF-----KHRSQF-----RNEASRE 286
QY 296 KKREKIHIPERSDAQRVF 314
Db 287 TNNSLITFGPEALAEQTVF 305
RESULT 5
CD80_RABIT
ID CD80_RABIT STANDARD; PRT; 299 AA.
AC P42070;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1

DE antigen).
GN CD80
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B/J X CHB:HM;
RX MEDLINE=95369849; PubMed=7642234;
RA Tsono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell
RT costimulatory molecules.";
RL Immunogenetics 42:217-220(1995).
CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D49843; BAA08643.1; -.
CC HSP: P33681; 1DR9.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_VHC.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00410; IG_like; 1.
DR Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 299 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT DOMAIN 33 243 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 244 264 POTENTIAL.
FT DOMAIN 265 299 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 122 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 154 222 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 49 115 POTENTIAL.
FT FT 161 215 POTENTIAL.
FT FT 52 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 299 AA; 33513 MW; 6744223E5CC91DE0 CRC64;

Query Match 14.0%; Score 243; DB 1; Length 299;
Best Local Similarity 25.8%; Pred. No. 1.3e-11;
Matches 81; Conservative 65; Mismatches 122; Indels 46; Gaps 14;

Qy 3 PQTGMLGNLFWAFLLSGAFLKIQAYFNETADLPFCFANSQNSLSELVWFWDQEN 62
Db 12 PRCLHLKCLLLALAGLHSSGISQVTSKVEAAALSCDY-NISIDELARMRIYWKDDQ 70
Qy 63 LVNLVEVLKGFDSVHSKYNGRTSP-SDSWTLRLHNLQIKDKLQCIHKKPTGMI 121
Db 71 MWLS-IISGQVE---VWPEYKQRTFPDIINLSLMTLALRLSDKGYTCVQKNENGSR 126
Qy 122 RIHQMSNELSVLANFSQPEIVPISNITENVYINLTCSSIHGYPEPK----KMSVLLRTKN 177

Db 127 REHLTSVTLISIRADFPVPSITDIGHDPNVK-RIRCSASGGFPPEPLAWMEDGELNAVN 185
Qy 178 STIEYDGIWQKSDQNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSSPSIELE 237
Db 186 ITVD-----QDLDTLYSSSELDLF---NVTNHRSIVCLIKYIGELS-VSQIFPWSKP 233
Qy 238 DPQPPDHPHIP-WITAVLPT----VIICVMVFLI---LWKWKKKPRNSYKCGTNTMER 289
Db 234 KQEPPIQLPFWV--IIPVSGALVLTAVLYCLACRHRVARWKRTR-----N 278
Qy 290 EESEQTKKREKIH 303
Db 279 EETVGTGRLSPIYL 292

RESULT 6
CD80 HUMAN STANDARD; PRT; 288 AA.
AC P33681;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1
DE antigen) (CTLA-4 counter-receptor B7.1) (B7) (BB1).
GN CD80 OR CD28LG1 OR CD28LG OR LAB7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=92307753; PubMed=2794510;
RA Freeman G.J., Freedman A.S., Segil J.M., Lee G., Whitman J.F.,
RA Nadler L.M.;
RT "B7, a new member of the Ig superfamily with unique expression on
RT activated and neoplastic B cells.";
RL J. Immunol. 143:2714-2722(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92307753; PubMed=1377173;
RA Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C.,
RA Dupont B.;
RT "Genomic organization and chromosomal location of the human gene
RT encoding the B-lymphocyte activation antigen B7.";
RL Immunogenetics 36:175-181(1992).
RN [3]
RP SEQUENCE OF 35-38.
RX MEDLINE=91341422; PubMed=1714935;
RA Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J.,
RA White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;
RT "Structure, expression, and T cell costimulatory activity of the
RT murine homologue of the human B lymphocyte activation antigen B7.";
RL J. Exp. Med. 174:625-631(1991).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=95088403; PubMed=7527824;
RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
RA Okumura K., Ito D., Azuma M.;
RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
RT cell proliferation, cytokine production, and generation of CTL.";
RL J. Immunol. 154:97-105(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 35-234.
RX MEDLINE=20125021; PubMed=10661405;
RA Ikemizu S., Gilbert R.J., Fennelly J.A., Collins A.V., Harlos K.,
RA Jones E.Y., Stuart D.I., Davis S.J.;
RT "Structure and dimerization of a soluble form of B7-1.";
RL Immunity 12:51-60(2000).
CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC RECEPTOR.

```

CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES
CC AND DENDRITIC CELLS.
CC -I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -I- DATABASE: NAME=PROW; NOTE=CD guide CD80 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd80.htm".
CC -----
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CC -----
DR EMBL; M27533; AAA36045.1; -
DR EMBL; M83077; AAA58390.1; -
DR EMBL; M83072; AAA58390.1; JOINED.
DR EMBL; M83073; AAA58390.1; JOINED.
DR EMBL; M83074; AAA58390.1; JOINED.
DR PIR; A45803; A45803.
DR PDB; 1DR9; 10-JAN-01.
DR Genew; HGNC:1700; CD80.
DR MIM; 112203; -
DR InterPro; IPR003599; Ig_MHC.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_Like; 1.
DR Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor; 3D-structure.
FT SIGNAL 1 34
FT CHAIN 35 288
FT DOMAIN 35 242 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT TRANSMEM 243 263 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 264 288 POTENTIAL.
FT DOMAIN 43 123 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 155 223 IG-LIKE V-TYPE DOMAIN.
FT DISULFID 50 116 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 162 216
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 288 AA; 33048 MW; B453BE3452B81F4 CRC64;
Query Match 11.6%; Score 201.5; DB 1; Length 288;
Best Local Similarity 25.1%; Pred. No. 1.8e-08;
Matches 78; Conservative 57; Mismatches 109; Indels 67; Gaps 17;
QY 14 FVMAFLSG-----AAPLQIAYENETADI.PCOFANSONQSISELV---VFMOQDENLVL 65
DB 19 FFOLLVLAGLHFCFSGVHVTKVEKVALTSC-----GHNVSVEBLATRIYQKEKQVNL 74
QY 66 NEVYLGEKFOVSHKSYNGRTSFD-SDSWTLRLHNLQIKDKGLYQCIIHHKPTGMIRIH 124
DB 75 TWM-----SGDMNINPKNRTIFDITNNLSIVILARPSDEGTVECVLVKYEKDAFKRH 130
QY 125 QMNSLSLVANFSOPEI-----VPSINTEVNVINLTCSIHGYEPKMSVL-----LRT 175
DB 131 LAEVLTVKADPTPSISDEIFTNIR-----RIICSTSGFPPEP-HLSWLENGELNA 184
QY 176 KNSTEYDGIWQKSGDNVTELYDVSISLVSPFDVTSNMFTFCILETDKTRLLSSPFSIE 235
DB 185 INTTV-----SDPETELYAVSGKLDP---NMTTNHSPMCLIKYGHLLR-VNQTFNNW 232

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QY 236 LEDPQPPDHI--PW---ITAVLPVLIICVMVRCLILMKWKKKBPNSYKCGTNTWRE 290
DB 233 TTQEHFPDNLPLPSWAITLISVNGIFVICLTYCF-----APR-----CRERR 275
QY 291 ESEQTKKREKI 301
DB 276 RNERL-RRESV 285

RESULT 7
BUTY_MOUSE
ID BUTY_MOUSE STANDARD; PRT; 524 AA.
AC Q62556; P97392;
DT 01-NOV-1997 (Rel. 35; Created)
DT 15-JUL-1998 (Rel. 36; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Butyrophillin precursor (BT).
GN BTN1AL OR BTN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary gland;
RX MEDLINE=97148936; PubMed=8995761;
RA Ogg S.L.; Komaragiri M.V.S.; Mather I.H.;
RT "Structural organization and mammary-specific expression of the
RT butyrophillin gene.";
RL Mamm. Genome 7:900-905 (1996).
RN [2]
RP SEQUENCE OF 39-487 FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=96125722; PubMed=8541302;
RA Ishii T.; Aoki N.; Noda A.; Adachi T.; Nakamura R.; Matsuda T.;
RT "Carboxy-terminal cytoplasmic domain of mouse butyrophillin
RT specifically associates with a 150-kDa protein of mammary epithelial
RT cells and milk fat globule membrane.";
RL Biochim. Biophys. Acta 1245:285-292 (1995).
CC -I- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC MEMBRANE (BY SIMILARITY).
CC -I- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
CC ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.
CC -I- DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING THE LAST HALF OF
CC PREGNANCY AND IS MAXIMAL DURING LACTATION.
CC -I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC SUBFAMILY.
CC -I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -----
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CC -----
DR EMBL; U67065; AAB51034.1; -
DR EMBL; S80642; AAB35893.1; -
DR MGD; MGI:103118; Btntlal.
DR InterPro; IPR001870; Gamma carboxylase.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR003878; SPRY domain.
DR InterPro; IPR003877; SPRY_receptor.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00622; SPRY; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00449; SPRY; 1.

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Oy 284 TMTWRESEFQTKREKTHI-----PERSDEAQRVFKSKTSSCDKS 325
Db 284 -SSKRLLEBKWKATLHADVDTLDPDTAHPHLFLYEDSKSVRLDS 330

RESULT 10
ID ICOL HUMAN STANDARD; PRT; 302 AA.
AC 075144; Q9NRQ1; Q9HD18;
DT 18-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ICOS ligand precursor [B7 homolog 2] (B7-H2) [B7-like protein G150]
DE (B7-related protein-1) (B7RP-1).
GN ICOSL OR B7H2 OR B7RP1 OR KIAA0653.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Dendritic cell;
RX MEDLINE=20477846; PubMed=11023515;
RA Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;
RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds
RT ICOS.";
RL Blood 96:2808-2813(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=20465019; PubMed=11007762;
RA Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K.,
RA Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H.,
RA Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;
RT "Characterization of a new human B7-related protein: B7RP-1 is the
RT ligand to the co-stimulatory protein ICOS.";
RL Int. Immunol. 12:1439-1447(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;
RX MEDLINE=20126021; PubMed=10657606;
RA Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,
RA Leonard J.P., Hunter S.B., Zollner R., Thomas J.L., Miyashiro J.S.,
RA Jacobs K.A., Collins M.;
RT "Identification of GL50, a novel B7-like protein that functionally
RT binds to ICOS receptor.";
RL J. Immunol. 164:1653-1657(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Ling V., Dunussi-Joannopolous K.;
RT "GL150 molecules and uses thereof.";
RL Patent number WO0121796, 29-MAR-2001.
CC -!- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
CC STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.

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CC -!- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,
CC KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE
CC MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES,
CC SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN
CC LYMPH NODES, LEUKOCYTES AND SPLEEN.
CC -!- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY
CC TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND
CC MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- CAUTION: Ref. 4 sequence differs from that shown in position 300
CC onward for an unknown reason.
CC -----
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CC -----
CC EMBL; AF199028; AAF34739.1; -.
CC EMBL; AF289028; AAG01176.1; -.
CC EMBL; AF216749; AAK16241.1; -.
CC EMBL; AB014553; BAA31628.1; ALT_SEQ.
CC EMBL; AX100595; CAC36465.1; -.
CC MIM; 605717; -.
CC DR InterPro; IPR003599; Ig.
CC DR InterPro; IPR003006; Ig_MHC.
CC DR InterPro; IPR003600; Ig_like.
CC Pfam; PF00047; Ig; 2.
CC SMART; SM00409; Ig; 1.
CC SMART; SM00410; Ig_like; 1.
CC B-cell activation; Immune response; Glycoprotein;
CC Immunoglobulin domain; Signal; Transmembrane; Multigene family;
CC Alternative splicing.
CC SIGNAL 1 18
CC CHAIN 19 302
CC DOMAIN 19 256
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 257 277
CC CYTOPLASMIC (POTENTIAL).
CC DOMAIN 30 120
CC IG-LIKE V-TYPE DOMAIN.
CC DOMAIN 151 223
CC IG-LIKE C2-TYPE DOMAIN.
CC DISULFID 37 113
CC POTENTIAL.
CC DISULFID 158 216
CC POTENTIAL.
CC CARBOHYD 70 70
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 137 137
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 173 173
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 186 186
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 225 225
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC VARSPLIC 300 302
CC GHV -> ESMNLLLLLS (IN ISOFORM 2).
CC SEQUENCE 302 AA; 33349 MW; 647934E21B5E34A CRC64;
CC
CC Query Match 9.5%; Score 165.5; DB 1; Length 302;
CC Best Local Similarity 21.7%; Pred. No. 1.le-05;
CC Matches 65; Conservative 61; Mismatches 121; Indels 53; Gaps 13;
CC
Oy 7 MGLSNILFVM-AFLLSGAAPLKIQAYFNETADLPQCFANSQNSLSLVVFWQDQENLVL 65
Db 3 LGSPGLFLFLFSLRADTQEKVRAMVSGDSVLSLSCAPEGSFRDLNDVYVYVWQTSKTV 62
Oy 66 NEVYLGG-KKEDSVHVKYMGRTSFD-----SDSWTLRLHLNLIQIKDKGLYOCIIHHKKPTG 119
Db 63 VTYHHPQNSSLEUVDSYRNEALMSAGMLRGDFSLRLFNVTTPDEQKFHCLV-LSQSIG 121
Oy 120 MIRIHHMNSLSVLANSQPEIVPTISNITENVYINLTCSHIGHPKPKMSVLLRTKST 179
Db 122 FQEVLSVEVTLHVAANFSP-VVSAPHSPSQDELFTTCTCTSGINGYPRP-NVYIWKNTDNL 179
Oy 180 IEVDGIMQKSD-----NVTELYDVSISSVSFPDVTNSMTIFCILET----- 222

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DR	InterPro; IPRO03596; Ig_v.	
DR	InterPro; IPRO03878; SPRY_domain.	
DR	InterPro; IPRO03877; SPRY_receptor.	
DR	Pfam; PF00047; ig; 1.	
DR	Pfam; PF00622; SPRY; 1.	
DR	SMART; SM00406; IGV; 1.	
DR	SMART; SM00449; SPRY; 1.	
KW	Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.	
FT	SIGNAL 1 26	
FT	CHAIN 27 526	BUTYROPHILIN.
FT	DOMAIN 27 242	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 243 269	POTENTIAL.
FT	DOMAIN 270 526	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD 55 55	N-LINKED (GLCNAC. .) (COMPLEX).
FT	CARBOHYD 215 215	N-LINKED (GLCNAC. .) (HYBRID).
FT	CONFLICT 35 35	Q -> P (IN REF. 3).
FT	CONFLICT 230 230	E -> D (IN REF. 1).
FT	SEQUENCE 526 AA; 59276 MW; A14126802BD19284 CRC64;	
QY	Query Match	9.3%; Score 162; DB 1; Length 526;
QY	Best Local Similarity	23.0%; Pred. No. 4.1e-05;
QY	Matches 80; Conservative 61; Mismatches 155; Indels 52; Gaps	
QY	5 CTMGLSNILFWAFILSGAFL-----KIQAFNETADLPFCOFANSQNSLSLVVFW 57	
DB	8 CIAGCLLFILOLPKDSAFPDIQVIGPEPIAVVGEDAEPLCL--SPNVSAKGMELRW 65	
QY	58 ODQENLVINEYL-----GKEKFDVSHSKYMGRTSFDS-----SWTLRLHNLQIKDKGLYQ 109	
DB	66 FREK--VSPAIVFSREGQEGEEMAEYRGVSLVEDHIAEGSVAVRIQEVKASDDGEYR 129	
QY	110 CIIHHKPTGMIRIHMNSSELSVLANSQEPILVPIFNITENVYINLTCSIIHGYEPKKM 169	
DB	124 CFFRODENEYEAIVH-----LKVAAIGSDPHI--SMKVOESGEIQLECTSVGWYEPQ-- 179	
QY	170 SYLLFTKNSITIEDGIMQKSDQNTVELDYSLISLSPFDTNSMTIFCIETDKTRLIS 229	
DB	175 -VQWRTHRGE-EPPSSESERNPDEGLF--TVRASVIIRDSSMKNVSCCI---RNLLLG 226	
QY	230 SPFSLELEDQPP-PPDHPFWITAV-LPTVLCVMVFCILMKWK---KKKPRNSYKCG 289	
DB	227 QEKEVEVSIIPASFFPLPFWVAVILVVLGLLTIGISFTWLYKERSRRRNEF---289	
QY	284 TMTWEREESQTKREKIH-----PERSDAQRVFKSSKTSCKDS 325	
DB	284 --SSKEKLEELKWKATLHADVDTLDPDTAHPHLFLYEDSKSVRLDS 330	
RESULT 12		
OX2G_HUMAN		
ID	OX2G_HUMAN	STANDARD; PRT; 274 AA.
AC	P41217;	
CD	01-FEB-1995 (Rel. 31, Created)	
DT	01-FEB-1995 (Rel. 31, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
GN	OX-2 membrane glycoprotein precursor (Fragment).	
GN	NOX2.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Theria; Primates; Catarrhini; Hominidae; Homo.	
ON	NCBI_TaxID=9606;	
RN	[1]	
RC	SEQUENCE FROM N.A.	
RC	TISSUE=Blood;	
RA	MEDLINE=87192943; PubMed=3032785;	
RX	McCaughan G.W.; Clack M.J.; Barclay A.N.;	
RT	"Characterisation of the human homolog of the rat MRC OX-2 membrane	
RT	glycoprotein."	
RL	Immunogenetics 25:329-335(1987).	
CC	!- SUBCELLULAR LOCATION: Type I membrane protein.	
CC	!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.	
CC	!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.	
CC	!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.	


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CC -----
DR EMBL; X05323; CAA28943.1; ALT SEQ.
DR EMBL; X05324; CAA28943.1; JOINED.
DR EMBL; X05325; CAA28943.1; JOINED.
DR EMBL; X05326; CAA28943.1; JOINED.
DR PIR; A47639; A47639.
DR Genew; HGNC:7203; MOX2.
DR MIM; 155970; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; ig; 1.
DR SMART; SM00410; ig_Like; 1.
DR Transmembrane; Glycoprotein; Neurone; B-cell; T-cell; Antigen;
KW Immunoglobulin domain; Signal.
FT NON_TER 1 1
FT SIGNAL <1 26 . POTENTIAL.
FT CHAIN 27 274 OX-2 MEMBRANE GLYCOPROTEIN.
FT DOMAIN 27 228 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 229 235 POTENTIAL..
FT DOMAIN 256 274 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 137 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 138 228 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 47 117 POTENTIAL.
FT DISULFID 156 210 POTENTIAL.
FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 99 99 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 274 AA; 30739 MW; 0A9547B48ED8979C CRC64;

Query Match 7.4%; Score 128; DB 1; Length 274;
Best Local Similarity 21.1%; Pred. No. 0.0071;
Matches 63; Conservative 57; Mismatches 120; Indels 58; Gaps 16;

QY 11 NILFWMAFLLSGAAPLKI-----QAYFNETADLPQCFANSQNSLSLVVFWQDQ-- 60
Db 13 SLVWVMAAVLCTAQVQVVTQDEREQLY--TTASLKCQLNAQ---EALIVTWQKKAV 66

QY 61 --ENLVL-----NEVYLKKEKFSVHSKYMGRTSFSDSWTLRLHNLQIKDKGLY 114
Dd 67 SPENNVTFSENHGVIQPAYKDKNITQGLQNSITTFW-----NTLEDEGCYMLFN- 120

QY 115 KKPTGMIRIHOMNSLSVLANSFQPEIVPISNITENVYINLTCSIHGYPPPKMSVLLR 174
Dd 121 --TFGCKI----SGTACLTVVVQV-IVSLHYKFSDEHLNITCSAT-ARAP--MVFWK 169

QY 175 TKNSTIEYDGMQSDQNTVELYDVISLSVSPFDVTSNMTIFC-ILE-----TKTRLSS 229
Dd 170 VPRSGIENSTVLUSHPNGTSTVTSI---LHKDPKQVQKEVTCVQLHGLVTFDFKQTVN 226

QY 230 SPFSIELEDPQPPPHIPWITAVPTVICVMVFLIKWKKKPRNSYKCGTNTM 287
Dd 227 KGYWFS-----VPLLISVSLVILLIISILLYMK-RHRNDRGELSGQGVQM 273

RESULT 13
OX2G_RAT STANDARD; PRT; 278 AA.
AC P04218;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
```

```
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE OX-2 membrane glycoprotein precursor (MRC OX-2 antigen).
GN MOX2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
CC [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85257428; PubMed=2862025;
RX Clark M.J., Gagnon J., Williams A.F., Barclay A.N.;
RT "MRC OX-2 antigen: a lymphoid/neuronal membrane glycoprotein with a
RT structure like a single immunoglobulin light chain.";
RL EMBO J. 4:113-118(1985).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: FOUND ON THE SURFACE OF NEURONES, THYMOCYTES,
CC B-CELLS, AND FOLLICULAR DENDRITIC CELLS.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
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CC -----
DR EMBL; X01785; CAA25925.1; -.
DR PIR; A02114; TDRTOX.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IgV; 1.
DR Transmembrane; Glycoprotein; Neurone; B-cell; T-cell; Antigen;
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 278 OX-2 MEMBRANE GLYCOPROTEIN.
FT DOMAIN 31 232 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 233 259 POTENTIAL.
FT DOMAIN 260 278 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 141 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 142 232 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 51 121 POTENTIAL.
FT DISULFID 160 214 POTENTIAL.
FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 278 AA; 31088 MW; BSA72DBE7B3116CD CRC64;

Query Match 7.4%; Score 128; DB 1; Length 278;
Best Local Similarity 22.1%; Pred. No. 0.0073;
Matches 70; Conservative 53; Mismatches 128; Indels 66; Gaps 16;

QY 3 PCTWGLSNILFWMAFLLSGAAPLKI-----QAYFNETADLPQCFANSQNSLSLVVFW 57
Dd 9 PCHLSTVSLWLAIAAVALSTAQVEVVTQDERKLLHTTASLRCSLKTTQ-----EPLIVTW 64

QY 58 QDQ-----ENLV-----LNEVYLKKEKFSVHSKYMGRTSFSDSWTLRLHNLQIKDKGLY 108
Dd 65 QKKKAVGPNVNVTSKAGVVIQPTVKORINITELGLLNTSITFW-----NTLDDGCGY 119

QY 109 QCIHHKPTGMIRIHOMNSLSVLANSFQPEIVPISNITENVYINLTCSIHGYPEPK 168
Dd 120 MCLF--NMFGSGKV-----SGTACLTVVVQVIVHLHVNRYFED-HLNITCSAT-ARAP-- 168

QY 169 MSVLLRTKNSTIEYDGMQSDQNTVELYDVISLSVSPFDVTSNMTIFCIL-----ETD 223
Dd 169 -AISWKGTSGGIE-NSTESHSGNGTT--SVTSLILRVKDKPTQVGKEVICQVLYLGNVID 224
```

QY 224 KTRLSSPFSIELEDPQPDHPHWITAVLPTVICVMVFCILIMKWKKKRPNRSYKCG 283
 Db 225 YKQSLDKGFWS-----VPLLISIVSLVILVILISILLYW-----KRRN----- 264

QY 284 TNTWEREESQTKREK 300
 Db 265 ---QERGSSQGMK 278

RESULT 14
 CXAR_MOUSE
 ID CXAR_MOUSE STANDARD; PRT; 365 AA.
 AC P97792; O09052;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coxsackievirus and adenovirus receptor homolog precursor (mCAR).
 GN CXADR OR CAR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=97190109; PubMed=9036860;
 RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
 RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
 RT "Isolation of a common receptor for Coxsackie B viruses and
 RT adenoviruses 2 and 5.";
 RL Science 275:1320-1323(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/MAI;
 RX MEDLINE=97450341; PubMed=9096397;
 RA Tomko R.P., Xu R., Philipson L.;
 RT "HCAR and mCAR: the human and mouse cellular receptors for subgroup C
 RT adenoviruses and group B coxsackieviruses.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RA Bergelson J.M., Krithivas A., Crowell T.L., Finberg R.W.;
 RT "The murine CAR homologue (mCAR) is a receptor for coxsackie B
 RT viruses and adenoviruses.";
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -|- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -|- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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 CC -----
 DR EMBL; Y10320; CAAT71368.1; -;
 DR EMBL; U90715; AAC53148.1; -;
 DR EMBL; Y11929; CAA72679.1; -;
 DR MGD; MGI:1201679; Cxadr.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_C2.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00410; Ig-like; 1.
 DR SMART; SM00408; IGC2; 1.
 KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 FT SIGNAL . 1 19 POTENTIAL.
 FT CHAIN . 20 365 COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR

FT DOMAIN 20 237 HOMOLOG.
 FT TRANSMEM 238 258 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 259 365 POTENTIAL.
 FT DOMAIN 34 127 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 155 219 IG-LIKE C2-TYPE DOMAIN 1.
 FT DISULFID 41 120 IG-LIKE C2-TYPE DOMAIN 2.
 FT DISULFID 162 212 BY SIMILARITY.
 FT CARBOHYD 106 106 BY SIMILARITY.
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 340 365 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VV (IN REF. 2 AND 3).
 SQ SEQUENCE 365 AA; 39947 MW; 5445B4B52A34B2A2 CRC64;

Query Match 7.2%; Score 124.5; DB 1; Length 365;
 Best Local Similarity 24.6%; Pred. No. 0.019;
 Matches 78; Conservative 49; Mismatches 125; Indels 65; Gaps 17;

QY 27 KIQAYFNETADLPQFANS-QNQSLSLVVFWQDQENLVLEV---YLCKEKFDSVHSKY 82
 Db 28 RIEKAKGETAYLCKFTLSPEDQGLDIEWLISPSDNQIVDQVILYSGDKIYDNYPD 87
 QY 83 MGRTSFDS-----SWTLRLHLNLOIKDGLYQCIHHKPTGMIRIHMNSLSVLANFS 137
 Db 88 KGRVHFTSNDVKSGDASINVNLQLSDIGTYQCKV--KKAQG---VANKKFLTLVLKPS 142
 QY 138 QPE-IVPISNITENVVINTCSSIHGYPEPKMSVLLRTKNSTIEVDGIMQKSDQNV 194
 Db 143 GTRCFVDSGEIENDP-KLKC-----EPKESGLPQFE-----WQKLSDSQTMP 185
 QY 195 -----ELYDVSISLSVSPDPVTNNMTIFCILETDKTRLLSSPFSIELEDP 249
 Db 186 TPWLAEMTSPVISVKNASSEYSG--TYSC---TVQNRVSGDQCMLRL-DVVPSPNAGTI 239
 QY 250 T-AVLPTVVICVMV-----FCLILMKWKKKRPNRSYKCGTNTWEREESQTKREK 304
 Db 240 AGAVIGTLLALVILGAILFCC-----HRKREEKY-----EKEVHHDIREDVPPP 284
 QY 305 ERSDAQRVFKSKTS 321
 Db 285 KSRTSTARSYIGSNHSS 301

RESULT 15
 TACT HUMAN
 ID TACT HUMAN STANDARD; PRT; 569 AA.
 AC P40200;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE T-cell surface protein tactile precursor (CD96 antigen).
 GN CD96.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92218864; PubMed=1313846;
 RA Wang P.L., O'Farrell S., Clayberger C., Krensky A.M.;
 RT "Identification and molecular cloning of tactile. A novel human T
 RT cell activation antigen that is a member of the Ig gene
 RT superfamily.";
 RL J. Immunol. 148:2600-2608(1992).
 CC -|- FUNCTION: MAY BE INVOLVED IN ADHESIVE INTERACTIONS OF ACTIVATED T
 CC AND NK CELLS DURING THE LATE PHASE OF THE IMMUNE RESPONSE. MAY
 CC FUNCTION AT A TIME AFTER T AND NK CELLS HAVE PENETRATED THE
 CC ENDOTHELIUM USING INTEGRINS AND SELECTINS, WHEN THEY ARE ACTIVELY
 CC ENGAGING DISEASED CELLS AND MOVING WITHIN AREAS OF INFLAMMATION.
 CC -|- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -|- TISSUE SPECIFICITY: EXPRESSED ON NORMAL T CELL LINES AND CLONES,
 CC AND SOME TRANSFORMED T CELLS, BUT NO OTHER CULTURED CELL LINES.

CC TESTED. IT IS EXPRESSED AT VERY LOW LEVELS ON ACTIVATED B CELLS.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED AT LOW LEVELS ON PERIPHERAL T CELLS.
CC AND IS STRONGLY UP-REGULATED AFTER ACTIVATION, PEAKING 6 TO 9 DAYS
CC AFTER THE ACTIVATING STIMULUS.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- DATABASE: NAME=PRO; NOTE=CD guide CD96 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd96.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M88282; AAA36662.1; -;
DR PIR; A46462; A46462;
DR InterPro; IPR003599; IG;
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 1.
KW Immunoglobulin domain; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 569 T-CELL SURFACE PROTEIN TACTILE.
FT DOMAIN 22 501 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 502 525 POTENTIAL.
FT DOMAIN 526 569 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 354 486 PRO/SER/THR-RICH.
FT DOMAIN 538 547 PRO-RICH.
FT DOMAIN 38 125 IG-LIKE V-TYPE DOMAIN 1.
FT DOMAIN 156 238 IG-LIKE V-TYPE DOMAIN 2.
FT DOMAIN 267 346 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 45 118 PROBABLE.
FT DISULFID 163 231 PROBABLE.
FT DISULFID 274 339 PROBABLE.
FT CARBOHYD 42 42 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 107 107 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 419 419 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 481 481 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 569 AA; 63887 MW; DF2F3BEE356F3BF2 CRC64;
Query Match 7.2%; Score 124; DB 1; Length 569;
Best Local Similarity 25.3%; Pred. No. 0.037;
Matches 63; Conservative 44; Mismatches 96; Indels 46; Gaps 15;
QY 28 IQAYFNETADLPQFANSONQSLSELVVFQDQENLVNEVLGKGFDSVSHKYMGRTS 87
DB 151 IEIETNQLEIPC-FQNSSSKISSEFTYAMSVEDN-GTOETLISQNHLSITLLKDRVK 208
QY 88 FDSDSWTLRLHNIQIKDKG-LYQCIHHKPTGMIRIHWNSGELSVLANFSQPEI-VPIS 145
DB 209 LGTD-YELHLSVPQIFDDCKESCHIR-----VGPENKILRSSTTVKV---FAKPEIPVIVE 260
QY 146 NITENVVI--NLTCSHIGYEPKPKMSVLLRTKNSTI--EYDGIM-----OKSQDNVTEL 196
DB 261 NNSTDVLEVRERFTCLLKNVFP---KANITWFDGSLHDEKEGIYITNEERKKGDFLEL 317
QY 197 YDVSISLSVSFPDVTNMTIFCI-----LETDK-TRLLSS-----PFISI-- 234

DB 318 KSVLTVHSNKPAQSDNLTWCWALSVPVGNKVMNISSEKITFLGSEISSTDPPLSVTE 377
QY 235 ELEDQPPPP 243
DB 378 STLDTPQSP 386
Search completed: February 13, 2003, 11:31:39
Job time : 19.5329 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 11:28:39 ; Search time 29.3934 Seconds
(without alignments)
2306.282 Million cell updates/sec

Title: US-09-425-516-2

Perfect score: 1733

Sequence: 1 MDPQCTMGLSNILFVMAFL.....AQRVFKSKTSSCDKSDTCF 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_todent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1615	93.2	323	6 Q9BDM4	Q9BDM4 macaca mula
2	1606	92.7	323	6 Q9BDB8	Q9BDB8 cercocebus
3	1597	92.2	323	6 Q9BDM9	Q9BDM9 macaca neme
4	1576	90.9	323	6 Q9BDM2	Q9BDM2 cercopithec
5	1303	75.2	275	6 Q9BDM9	Q9BDM9 papio anubi
6	1003	57.9	329	6 Q9TTF2	Q9TTF2 canis fami
7	953	55.0	325	6 O02838	O02838 sus scrofa
8	913	52.7	332	6 Q9GMZ7	Q9GMZ7 felis silve
9	912	52.6	332	6 Q9SL16	Q9SL16 felis silve
10	903	52.1	329	6 Q9XSX6	Q9XSX6 felis silve
11	886.5	51.2	280	6 Q9TTF1	Q9TTF1 canis fami
12	801.5	46.2	284	6 Q9GL33	Q9GL33 bos taurus
13	731.5	42.2	309	11 Q91YV7	Q91YV7 mus musculu
14	724.5	41.8	314	11 Q61238	Q61238 mus musculu
15	715.5	41.3	356	11 Q64381	Q64381 mus musculu
16	702.5	40.5	313	11 O35531	O35531 rattus norv

17	453	26.1	149	11	Q62810	Q62810 rattus norv
18	243	14.0	306	11	Q9R1Z9	Q9R1Z9 mus musculu
19	231	13.3	296	6	O46405	O46405 bos taurus
20	224	12.9	292	6	Q9GMZ8	Q9GMZ8 felis silve
21	224	12.9	292	6	O02758	O02758 felis silve
22	222	12.8	321	11	Q62624	Q62624 rattus norv
23	222	12.8	321	11	O55202	O55202 rattus norv
24	220	12.7	321	11	O35187	O35187 rattus norv
25	211	12.2	290	11	Q62680	Q62680 rattus norv
26	204.5	11.8	288	6	O77684	O77684 macaca neme
27	199.5	11.5	288	6	O28499	O28499 macaca mula
28	199.5	11.5	304	6	Q9TQX1	Q9TQX1 canis fami
29	187.5	10.8	288	6	Q9BDM6	Q9BDM6 cercocebus
30	187.5	10.8	289	6	Q28347	Q28347 cercocebus
31	187.5	10.8	296	13	O42404	O42404 gallus gall
32	187	10.8	296	6	Q8WMZ2	Q8WMZ2 sus scrofa
33	186.5	10.8	288	6	Q9TTF0	Q9TTF0 sus scrofa
34	186.5	10.8	297	6	O9BE99	O9BE99 sus scrofa
35	185.5	10.7	316	11	O8VE98	O8VE98 mus musculu
36	185	10.7	229	6	Q9TTF1	Q9TTF1 sus scrofa
37	185	10.7	230	6	Q9N213	Q9N213 sus scrofa
38	183	10.6	235	6	O9N0T0	O9N0T0 canis fami
39	183	10.6	235	6	Q9TQS8	Q9TQS8 canis fami
40	181.5	10.5	316	4	O9BXR1	O9BXR1 homo sapien
41	179	10.3	524	11	Q921K7	Q921K7 mus musculu
42	176.5	10.2	290	11	O9EP73	O9EP73 mus musculu
43	176.5	10.2	334	4	Q9NR44	Q9NR44 homo sapien
44	175.5	10.1	334	4	Q9BU81	Q9BU81 homo sapien
45	175.5	10.1	359	4	P78410	P78410 homo sapien

ALIGNMENTS

RESULT 1

Q9BDM4 PRELIMINARY; PRT; 323 AA.
AC Q9BDM4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CD86 protein precursor.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villingger F., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344857; AAK37540.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 323 AA; 37019 MW; D211E103DB1A7D7A CRC64;

Query Match 93.2%; Score 1615; DB 6; Length 323;

Best Local Similarity 94.4%; Pred. No. 3.5e-128; Mismatches 6; Indels 0; Gaps 0;

Matches 305; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 7 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSQNSLSLVVFWQDNVLN 66

Db 1 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSQNSLSLSLVVFWQDNVLN 60

QY 67 EYVLGKEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRIHQM 126

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Db 61 EVYLGKFKDPSVHSGYMGRTSFDPESWTLRLHNLQIKDKGLYQCIIHHKRTGMRIRHQM 120
|||||
Qy 127 NSELVLANFSQPEIPIVPSNITENVYINLTCSIIHGYPKPKMSVLLRTKNSITIEDGIM 186
|||||
Db 121 NSELVLANFSQPEIPIVPSNITENVYINLTCSIIHGYPKPKMSVLLRTKNSITIEDGIM 180
|||||
Qy 187 QKSDQNVTELYDVSISSLSVSPDPVTSNMNITFCILETDKTRLLSSPFSIELEDPOPPDHI 246
|||||
Db 181 QKSDQNVTELYDVSISSLSVSPDPVTSNMNITFCILETDKTRLLSSPFSIELEDPOPPDHI 240
|||||
Qy 247 PWITAVLPTVVICVMVFCILWKKKKRPNRSYKCGTNTMERESSEOTKKREKIHIPER 306
|||||
Db 241 PWITAVLPTVVICVMVFCILWKKKKRPNRSYKCGTNTMERESSEOTKKREKIHIPER 300
|||||
Qy 307 SDEAQRVFKSSKTSKSDKSDTCF 329
|||||
Db 301 SDEAQCQVFKSLKTPSCDKSDTRF 323
|||||

RESULT 2
Q9BDB8 PRELIMINARY; PRT; 323 AA.
AC Q9BDB8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CD86 protein precursor.
OS Carcocebus torquatus acys (Red-crowned mangabey) (sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecinae; Cercopithecidae;
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL: AF344840; AAK37536.1; -.
DR InterPro: IPR003599; IG_.
DR InterPro: IPR003596; IG_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
KW Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 323 CD86 PROTEIN.
FT VARIANT 26 26 F -> L.
FT VARIANT 97 97 K -> R.
FT VARIANT 138 138 I -> T.
FT VARIANT 147 147 I -> V.
FT VARIANT 166 166 L -> S.
FT VARIANT 172 172 P -> S.
FT VARIANT 206 206 S -> C.
FT VARIANT 260 260 I -> T.
FT VARIANT 284 284 E -> V.
FT VARIANT 319 319 S -> T.
FT VARIANT 322 322 H -> R.
SQ SEQUENCE 323 AA; 37010 MW; 45B217C606A79B75 CRC64;

Query Match 92.7%; Score 1606; DB 6; Length 323;
Best Local Similarity 93.8%; Pred. No. 2e-127;
Matches 303; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

Qy 7 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSONOSLSLSELYVFWQDENLVN 66
|||||
Db 1 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSONOSLSLSELYVFWQDENLVN 60
|||||
Qy 67 EVYLGKFKDPSVHSGYMGRTSFDPESWTLRLHNLQIKDKGLYQCIIHHKRTGMRIRHQM 126
|||||
Db 61 EVYLGKFKDPSVHSGYMGRTSFDPESWTLRLHNLQIKDKGLYQCIIHHKRTGMRIRHQM 120
|||||

Query Match 92.7%; Score 1606; DB 6; Length 323;
Best Local Similarity 93.8%; Pred. No. 2e-127;
Matches 303; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy 127 NSELVLANFSQPEIPIVPSNITENVYINLTCSIIHGYPKPKMSVLLRTKNSITIEDGIM 186
|||||
Db 121 NSELVLANFSQPEIPIVPSNITENVYINLTCSIIHGYPKPKMSVLLRTKNSITIEDGIM 180
|||||
Qy 187 QKSDQNVTELYDVSISSLSVSPDPVTSNMNITFCILETDKTRLLSSPFSIELEDPOPPDHI 246
|||||
Db 181 QKSDQNVTELYDVSISSLSVSPDPVTSNMNITFCILETDKTRLLSSPFSIELEDPOPPDHI 240
|||||
Qy 247 PWITAVLPTVVICVMVFCILWKKKKRPNRSYKCGTNTMERESSEOTKKREKIHIPER 306
|||||
Db 241 PWITAVLPTVVICVMVFCILWKKKKRPNRSYKCGTNTMERESSEOTKKREKIHIPER 300
|||||
Qy 307 SDEAQRVFKSSKTSKSDKSDTCF 329
|||||
Db 301 SDEAQCQVFKSLKTPSCDKSDTHF 323
|||||

RESULT 3
Q9BDM9 PRELIMINARY; PRT; 323 AA.
AC Q9BDM9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CD86 protein precursor.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL: AF344851; AAK37611.1; -.
DR InterPro: IPR003599; IG_.
DR InterPro: IPR003596; IG_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
KW Signal.
FT SIGNAL 1 17 POTENTIAL.
FT SIGNAL 1 17 POTENTIAL.
SQ SEQUENCE 323 AA; 37079 MW; C6CB82F125C647FD CRC64;

Query Match 92.2%; Score 1597; DB 6; Length 323;
Best Local Similarity 93.2%; Pred. No. 1.1e-126;
Matches 301; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Qy 7 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSONOSLSLSELYVFWQDENLVN 66
|||||
Db 1 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSONOSLSLSELYVFWQDENLVN 60
|||||
Qy 67 EVYLGKFKDPSVHSGYMGRTSFDPESWTLRLHNLQIKDKGLYQCIIHHKRTGMRIRHQM 126
|||||
Db 61 EVYLGKFKDPSVHSGYMGRTSFDPESWTLRLHNLQIKDKGLYQCIIHHKRTGMRIRHQM 120
|||||

Query Match 92.2%; Score 1597; DB 6; Length 323;
Best Local Similarity 93.2%; Pred. No. 1.1e-126;
Matches 301; Conservative 14; Mismatches 8; Indels 0; Gaps 0;
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Db 301 SDEAQCVRKSLKTPSCDKSDTRF 323
||||| ||||| || ||||| ||
RESULT 4
Q9BDN2 ID Q9BDN2 PRELIMINARY; PRT; 323 AA.
AC Q9BDN2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CDB6 protein.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villingner F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344861; AAK37543.1; -.
DR InterPro; IPR003599; Ig_v.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SIGNAL.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 323 AA; 37045 MW; 3E43152A8FD17267 CRC64;
Query Match 90.9%; Score 1576; DB 6; Length 323;
Best Local Similarity 92.9%; Pred. No. 6.8e-125;
Matches 300; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
Qy 7 MGLSNILFVMAFLLSGAAPLKIQAIFYNETADLPCQFANSQNSLSLVVFWQENLVN 66
Db 1 MGLINILFVMAFLLSGAAPLKIQAIFYNETADLPCQFANSQNSLSLVVFWQENLVN 60
Qy 67 EVYLGKEKFDSDVSHSKYMGRTSFDPSWTLRLHNLQIKDKGLYQCIHHKKTGMIRI 126
Db 61 EVYLGKEKFDSDVSHSKYMGRTSFDPSWTLRLHNLQIKDKGLYQCIHHKKTGMIRI 120
Qy 127 NSELSVLANFSQPEIYVPIISNTENYINLTCSIIHGYPEPKMSVLLRTKNSITIEYD 186
Db 121 NSELSVLANFSQPEIYVPIISNTENYINLTCSIIHGYPEPKMSVLLRTKNSITIEYD 180
Qy 187 QKSQDNVTELYDVSISSVSFPDVTNNMTFCILETDKTRLLSSPFIETEDPQPPDHI 246
Db 181 QKSQDNVTELYDVSISSVSFPDVTNNMTFCILETDKTRLLSSPFIETEDPQPPDHI 240
Qy 247 PWITAVLPTVIIICVMVFCILILWKKKKPRNSYKCGTNTMEREESEQTKKREKIH 306
Db 241 PWITAVLPTVIIICVMVFCILILWKKKKPRNSYKCGTNTMEREESEQTKKREKIN 300
Qy 307 SDEAQRVFKSKTSCKSDCTCF 329
Db 301 SDETCQVFKSLKTPSCDKSDTRF 323
||||| ||||| ||||| ||
RESULT 5
Q9BDN9 ID Q9BDN9 PRELIMINARY; PRT; 275 AA.
AC Q9BDN9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CDB6 protein precursor.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.

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OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villingner F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344836; AAK37532.1; -.
DR InterPro; IPR003599; Ig_v.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SIGNAL.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 275 AA; 31343 MW; 3AAD3481B4F37C19 CRC64;
Query Match 75.2%; Score 1303; DB 6; Length 275;
Best Local Similarity 79.6%; Pred. No. 5.8e-102;
Matches 257; Conservative 13; Mismatches 5; Indels 48; Gaps 1;
Qy 7 MGLSNILFVMAFLLSGAAPLKIQAIFYNETADLPCQFANSQNSLSLVVFWQENLVN 66
Db 1 MGLSNILFVMAFLLSGAAPLKIQAIFYNETADLPCQFANSQNSLSLVVFWQENLVN 60
Qy 67 EVYLGKEKFDSDVSHSKYMGRTSFDPSWTLRLHNLQIKDKGLYQCIHHKKTGMIRI 126
Db 61 EVYLGKEKFDSDVSHSKYMGRTSFDPSWTLRLHNLQIKDKGLYQCIHHKKTGMIRI 120
Qy 127 NSELSVLANFSQPEIYVPIISNTENYINLTCSIIHGYPEPKMSVLLRTKNSITIEYD 186
Db 121 NSELSVLANFSQPEIYVPIISNTENYINLTCSIIHGYPEPKMSVLLRTKNSITIEYD 180
Qy 187 QKSQDNVTELYDVSISSVSFPDVTNNMTFCILETDKTRLLSSPFIETEDPQPPDHI 246
Db 181 QKSQDNVTELYDVSISSVSFPDVTNNMTFCILETDKTRLLSSPFIETEDPQPPDHI 228
Qy 247 PWITAVLPTVIIICVMVFCILILWKKKKPRNSYKCGTNTMEREESEQTKKREKIH 306
Db 229 -----GTNTMEREESEQTKKREKINVPER 252
Qy 307 SDEAQRVFKSKTSCKSDCTCF 329
Db 253 SDEAQCVRKSLKTPSCDKSDTRF 275
||||| ||||| ||||| ||
RESULT 6
Q9TTF2 ID Q9TTF2 PRELIMINARY; PRT; 329 AA.
AC Q9TTF2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE B7-2 protein.
GN CD86.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20093996; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
RT Molecules.";
RL Immunogenetics 50:349-353(1999).
DR EMBL; AF106826; AAF17297.1; -.
DR HSSP; P33681; 1DR9.
DR InterPro; IPR003006; Ig_MHC.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

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SQ SEQUENCE 329 AA; 37774 MW; D98BB63437BF7B73 CRC64;
Query Match 57.9%; Score 1003; DB 6; Length 329;
Best Local Similarity 62.3%; Pred. No. 1.4e-76;
Matches 205; Conservative 47; Mismatches 71; Indels 6; Gaps 6;

QY 4 OCTMGLSNILFYMAFLLSGAAPLKIQAYFNETADLPFCOFANSONQSLSLVFWQDQENL 63
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 RCTMELNNILFYMTLLYGAASMKSQAYFNKTGELPCHFTNSQNLSDLVFWQDQDKL 63
QY 64 VLNEVYLGEKFDVSVHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKPTGMIRI 123
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 VLVELYRGKENPQVHRKYKRTSFDKDNWTLRLHNLQIKDKGLYQCFVHHKPGKGLVPM 123
QY 124 HQMSLSVLANFSQPEIPIISNITENV-YINLTCSHIGYPEPKKMSVLLRTKNSITIEY 182
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 HQMSDLSVLANFSQPEIMVTSNRTENSGIINLTCSIIQGYPEPKMYFLVKTENSTKY 183
QY 183 DGIWOKSDQNVTELYDVSISVSFPDVTSTNMTIFCILETDKTRLLSPFSIELE-DPOP 241
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 DTVMKKSQNNVTELYNVSISLSFVSPB-ASNVSIFCVQLQESMKLPSLPYNIDAHKTPP 242
QY 242 PDHPITAVL-PTVIICVMVFCILILWKWKKKRPRNSYKCGTNTMERESSEQTKKREK 300
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 243 DGDHILWIAALLVMLVILCGMVFLTLRK-RKKKQPGPSHECETIKRKESQTKRVR 301
QY 301 IHIPERSDEAQRVFKSKTSKCDKSDTCF 329
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 302 YHETERSDEAQC-V-NILKTASGDSNTTQF 329

RESULT 7
O02838 PRELIMINARY; PRT; 325 AA.
AC O02838;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE B7-2.
DR EMBL; L76099; AAB61307.1; -.
DR InterPro; IPR003596; IG v.
DR SMART; SM00406; IGV; 1.
DR SUS SCROFA (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97047772; PubMed=8892613;
RA Maher S.E., Karmann K., Min W., Hughes C.C., Pober J.S.,
RA Bothwell A.L.;
RT "Porcine endothelial CD86 is a major costimulator of xenogeneic human
RT T cells: cloning, sequencing, and functional expression in human
RT endothelial cells.";
RL J. Immunol. 157:3838-3844 (1996).
DR EMBL; L76099; AAB61307.1; -.
DR InterPro; IPR003596; IG v.
DR SMART; SM00406; IGV; 1.
DR SEQUENCE 325 AA; 36527 MW; 988BE08137B0597D CRC64;

Query Match 55.0%; Score 953; DB 6; Length 325;
Best Local Similarity 61.4%; Pred. No. 2.3e-72;
Matches 202; Conservative 44; Mismatches 73; Indels 10; Gaps 8;

QY 7 MGLSNILFYMAFLLSGAAPLKIQAYFNETADLPFCOFANSONQSLSLVFWQDQENLVN 66
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGLSNILFYMWLLLSGAASLKSQAYFNETGELPCHFTNSQNLSDLVFWQDQNLVLY 60
QY 67 EYVLGEKFDVSVHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKPTGMIRI 126
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ELYRGQEKPHNVSKYMGRTSFDQATWTLRLHNLQIKDKGSYQCFFIHHKPGHGLVPIHQ 120
QY 127 NSLSVLANFSQPEIPIISNITENVYINLTCSHIGYPEPKKMSVLLRTKNSITIEYDGM 186
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 SSDLSVLANFSQPEIINLTNHTENSVINLTCSSTQGYPEPKMYMLLNTKNSITTEHADM 180
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QY 187 OKSDQNVTELYDVSISVSFPDVTSTNMTIFCI--LETDKTRLLSPFSIELEDP-OPP- 242
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 KKSQNNITELYNVSIRVSLPTTPET-NVSIVCVLQLEPSKTLFLSLPCNIDAKPVPQPV 239
QY 243 PDHPITAVLPT-VIICVMVFCILILWKWKKKRPRNSYKCG-TNTERESSEQTKKREK 300
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 PDHILWIAALLVTVVVMVSCVSVFLTLRK-RKKKQPGPSNECGETIKMKRKASEQTKNRAE 298
QY 301 IHIPERSDEAQRVFKSKTSKCDKSDTCF 329
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 299 VH--ERSDDAQCQDQVILKTASDINSITTDF 325

RESULT 8
O9GMZ7 PRELIMINARY; PRT; 332 AA.
AC O9GMZ7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE B7-2.
DR EMBL; AB030652; BAB11688.1; -.
DR InterPro; IPR003596; IG v.
DR SMART; SM00406; IGV; 1.
DR SEQUENCE 332 AA; 37812 MW; 672C8B3667D1E3C0 CRC64;

Query Match 52.7%; Score 913; DB 6; Length 332;
Best Local Similarity 58.7%; Pred. No. 5.6e-69;
Matches 193; Conservative 43; Mismatches 85; Indels 8; Gaps 7;

QY 6 TMGLSNILFYMAFLLSGAAPLKIQAYFNETADLPFCOFANSONQSLSLVFWQDQENLV 65
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 7 TMGLSHTLLVMALLLSGVSSMKSQAYFNKTGELPCHFTNSQNLSDLVFWQDQDKLV 66
QY 66 NEVYLGEKFDVSVHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKPTGMIRI 125
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 YEIPRGKENPQVHLKYKRTSFPDKNWTLLRLHNLQIKDKGYTHCFIHYKPGKGLVPMHQ 126
QY 126 MNSLSVLANFSQPEIPIISNITENV-YINLTCSHIGYPEPKKMSVLLRTKNSITIEYDG 184
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 127 MSDLSVLANFSQPEITVTSNRTENSGIINLTCSIIQGYPEPKMYFQINTENSTTKYDT 186
QY 185 IMQKSDQNVTELYDVSISVSFPDVTSTNMTIFCILETDKTR-LLSPFSIELE--DPQP 241
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 187 VMKKSQNNVTELYNVSISLSFVSPB-AHNVSVFCALKLETLEMLLSLPFNIDAKPKDKP 245
QY 242 PDHPITAVLPT-VIICVMVFCILILWKWKKKRPRNSYKCGTNTMERESSEQTKKREK 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 246 EQGHFWIAAVLVMFVFCGMVSFKTLRK-RKKKQPGPSHECETIKRKESQTKNERVP 304
QY 301 IHIPERSDEAQRVFKSKTSKCDKSDTCF 329
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 305 YHVPERSDEAQC-V-NILKTASGDSKSTTHF 332

RESULT 9
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Q95L16
ID Q95L16 PRELIMINARY; PRT; 332 AA.
AC Q95L16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CD86.
GN CD86.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21390213; PubMed=11498243;
RA Yang S., Sellins K.S., Powell T., Stoneman E., Sim G.K.;
RT "Novel transcripts encoding secreted forms of feline CD80 and CD86
costimulatory molecules.";
RL Vet. Immunol. Immunopathol. 81:15-21(2001).
DR EMBL; AY007704; AAG23342.1; -
SQ SEQUENCE 332 AA; 37826 MW; 8BFCB83667D1E3D8 CRC64;

Query Match 52.6%; Score 912; DB 6; Length 332;
Best Local Similarity 58.4%; Pred. No. 6.9e-69;
Matches 192; Conservative 44; Mismatches 85; Indels 8; Gaps 7;

QY 6 TMGLSNILFVMAFLLSGAAPLKIQAYENETADLPQFANSONQSLSELVVFWDQENLVL 65
DB 7 TMGLSHTLLVWALLLSGVSSMKSQAYFNKTGELPCHFTNSQNSISLDELVVFWDQDKLVL 66
QY 66 NEVYLKKEKFDVSVMKGRSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRIHQ 125
DB 67 YEIFRGKENPQNVHLKYKGRSFDKDNWTLRLHNVQIKDKGTYHCFIHYKPGKGLVPMHQ 126
QY 126 MNSLSVLANFSOPEIVPSNITENV-YINLTCSHGYPEPKMSVLLRTKNSITIEYDG 184
DB 127 MSSDLVLANFSOPEIVTSNRTENSGINLTCSHGYPEPKMYFQNTENSTTKYDT 186
QY 185 IMQKSDNVTLYDVVISLSVSPDVTNMTIFCILETDKTR-LLSSPFSIELE--DPQP 241
DB 187 VMKKSQNNVTLYNVSISLPSFVPE-AHNVSVFCALKLETLEMLLSLPPNIDAPKDKDP 245
QY 242 PPDHIPWITAVLPT-VIIICVMVFCILILWKKKKPRNSYKCGTNTMERESQTKKREK 300
DB 246 EQGHFLIAAVLVFVFCMVSKFYLTK-RKKQPGPSHECETIKRKESKOTNERVP 304
QY 301 IHIPERSDEAQRVFKSKTSCKDSKTS 329
DB 305 YHVPERSDEAQC-I-NILKTASGDKSTTHF 332

RESULT 10
Q95X56 PRELIMINARY; PRT; 329 AA.
AC Q95X56;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CD86 antigen.
GN CD86.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20180222; PubMed=10713336;
RA Choi I.S., Hsieh S.M., Winslow B.J., Collisson E.W.;
RT "Sequence analyses of feline B7 costimulatory molecules.";
RL Vet. Immunol. Immunopathol. 73:219-231(2000).
DR EMBL; AF157827; AAD42974.1; -
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGv; 1.
SQ SEQUENCE 329 AA; 37481 MW; A10621E3C00A08BB CRC64;

Query Match 51.2%; Score 886.5; DB 6; Length 280;
Best Local Similarity 55.7%; Pred. No. 7.9e-67;
Matches 182; Conservative 40; Mismatches 54; Indels 51; Gaps 4;

QY 4 OCTWGLSNILFVMAFLLSGAAPLKIQAYENETADLPQFANSONQSLSELVVFWDQENL 63
DB 4 RCTMELNLLVFWMTLLYGAASMKSQAYFNKTGELPCHFTNSQNSISLDELVVFWDQDKL 63
QY 64 VINEVYLKKEKFDVSVMKGRSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRI 123
DB 64 VLYELYRGKENPQNVHRKYKGRSFDKDNWTLRLHNLQIKDKGLYQCFVHKGKGLVPM 123
QY 124 HOMNSELVLANSOPEIVPSNITENV-YINLTCSHGYPEPKMSVLLRTKNSITIEY 182
DB 124 HOMNSELVLANSOPEIVPSNITENV-YINLTCSHGYPEPKMSVLLRTKNSITIEY 182

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SQ SEQUENCE 329 AA; 37481 MW; A10621E3C00A08BB CRC64;

Query Match 52.1%; Score 903; DB 6; Length 329;
Best Local Similarity 58.5%; Pred. No. 3.9e-68;
Matches 190; Conservative 44; Mismatches 83; Indels 8; Gaps 7;

QY 6 TMGLSNILFVMAFLLSGAAPLKIQAYENETADLPQFANSONQSLSELVVFWDQENLVL 65
DB 7 TMGLSHTLLVWALLLSGVSSMKSQAYFNKTGELPCHFTNSQNSISLDELVVFWDQDKLVL 66
QY 66 NEVYLKKEKFDVSVMKGRSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRIHQ 125
DB 67 YEIFRGKENPQNVHLKYKGRSFDKDNWTLRLHNVQIKDKGTYHCFIHYKPGKGLVPMHQ 126
QY 126 MNSLSVLANFSOPEIVPSNITENV-YINLTCSHGYPEPKMSVLLRTKNSITIEYDG 184
DB 127 MSSDLVLANFSOPEIVTSNRTENSGINLTCSHGYPEPKMYFQNTENSTTKYDT 186
QY 185 IMQKSDNVTLYDVVISLSVSPDVTNMTIFCILETDKTR-LLSSPFSIELE--DPQP 241
DB 187 VMKKSQNNVTLYNVSISLPSFVPE-AHNVSVFCALKLETLEMLLSLPPNIDAPKDKDP 245
QY 242 PPDHIPWITAVLPT-VIIICVMVFCILILWKKKKPRNSYKCGTNTMERESQTKKREK 300
DB 246 EQGHFLIAAVLVFVFCMVSKFYLTK-RKKQPGPSHECETIKRKESKOTNERVP 304
QY 301 IHIPERSDEAQRVFKSKTSCKDSKTS 325
DB 305 YHVPERSDEAQC-I-NILKTASGDKN 328

RESULT 11
Q95TFL PRELIMINARY; PRT; 280 AA.
AC Q95TFL;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Truncated B7-2 protein.
GN CD86.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20093996; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
Molecules.";
RL Immunogenetics 50:349-353(1999).
DR EMBL; AF106827; AAF17298.1; -
DR HSP; P33681; 1DR9.
DR InterPro; IPR003006; IG_MHC.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 280 AA; 32285 MW; 3C8EBCA4D826A7F3 CRC64;

Query Match 51.2%; Score 886.5; DB 6; Length 280;
Best Local Similarity 55.7%; Pred. No. 7.9e-67;
Matches 182; Conservative 40; Mismatches 54; Indels 51; Gaps 4;

QY 4 OCTWGLSNILFVMAFLLSGAAPLKIQAYENETADLPQFANSONQSLSELVVFWDQENL 63
DB 4 RCTMELNLLVFWMTLLYGAASMKSQAYFNKTGELPCHFTNSQNSISLDELVVFWDQDKL 63
QY 64 VINEVYLKKEKFDVSVMKGRSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRI 123
DB 64 VLYELYRGKENPQNVHRKYKGRSFDKDNWTLRLHNLQIKDKGLYQCFVHKGKGLVPM 123
QY 124 HOMNSELVLANSOPEIVPSNITENV-YINLTCSHGYPEPKMSVLLRTKNSITIEY 182
DB 124 HOMNSELVLANSOPEIVPSNITENV-YINLTCSHGYPEPKMSVLLRTKNSITIEY 182

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Db 124 HOMNSDLSVLANSFQPEIMVTSNRTENSIGINLTCSIIQGYPEPKMYFLVKTENSSTKY 183
QY 183 DGTMOXSDNVYDVSISLVSFPDVTSTNTIFCILETDKTRLLSPFSIEUDELQPP 242
Db 184 DTWKKSQNNVTLNVSISVSFVPE-ANVSIFCVLOESKMLPSLPYNIE----- 235
QY 243 PDHIPMITAVLPTVIICVMVFCILWLKWKXKXPRNSYKCGTNTWEREESQTKRKHIH 302
Db 236 -----TNKVEREESQTKRVRVYH 254
QY 303 IPRSDAORVFKSSKTSCKSDTCP 329
Db 255 ETERSDEAQC-V-NISKTAGSDNSTQF 280

RESULT 12
Q9GLJ33 PRELIMINARY; PRT; 284 AA.
AC Q9GLJ33; 2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CD86 antigen (Fragment).
OS CD86.
GN Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PERIPHERAL BLOOD;
RA Brooke G.P., Howard C.J., Parsons K.R.;
RT "Cloning and distribution of cattle CD86.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ291475; CAC13140.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003596; IG.v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
FT NON TER 284 284
SQ SEQUENCE 284 AA; 32021 MW; 797BB6639E297841 CRC64;

Query Match 46.2%; Score 801.5; DB 6; Length 284;
Best Local Similarity 58.1%; Pred. No. 1.2e-59;
Matches 165; Conservative 42; Mismatches 60; Indels 17; Gaps 7;

QY 4 OCTMGLSNILFVMAFL-----SQAAPLKIQAYFNETADLPCOFANSQNSLSLVF 56
Db 4 KCTMGLRNLGMALRLSVSKVPFSGAASLASHAFNETGELPCHFPNTQNLSDLVIF 63
QY 57 WQDQENLVNEVYLGEKEDSVHSKYMGRTSFDSWTLRLHNLQIKDKGLYQCIHHKK 116
Db 64 WQDQNKVLVLELFGQEKNNVNPYIGRTSFQDSWTLRLHNLQIKDKGLYQCIHRR 123
QY 117 PTGMIRIHMNSLSVLANSFQPEIVPISNITE--NVIYINLTCSIHGYPEPKMVSLLR 174
Db 124 SQGLVSIHOMSSDLIVLANSFQPEIRLIANQTEKSNIT-INTCSSIQGYPEPQRMVYSLN 182
QY 175 TKNSTIEVDGTMOXSDNVYDVSISLVSFPDVTSTNTIFCILETDKTR-LLSPPS 233
Db 183 ITNNSSTYDAVMKXSQNTIELNVSISVSFPFIPET-NVTIFCALQLEPTKILUSQPIN 241
QY 234 IELEDP---QPPDHPITAVLPTVIICVMVFCILWLKWKXKX 274
Db 242 IDAKSFVSPVPDPHILWIAALLVTVVSGMVFLTL--KKKKKK 283

RESULT 13
Q91YV7 PRELIMINARY; PRT; 309 AA.
AC Q91YV7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CD86 antigen.
GN CD86.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013807; AAH13807.1; -.
DR MGD; MGI:101773; Cd86.
SQ SEQUENCE 309 AA; 34714 MW; 61593C49EFCB0CE5 CRC64;

Query Match 42.2%; Score 731.5; DB 11; Length 309;
Best Local Similarity 51.1%; Pred. No. 1e-53;
Matches 157; Conservative 44; Mismatches 93; Indels 13; Gaps 5;

QY 1 MDPOCTMGLSNILFVMAFLSQAAPLKIQAYFNETADLPCOFANSQNSLSLVVFWDDQ 60
Db 1 MDPRCTMGLAILFVTLISDAVSVEIQAYFNGTAYLPCPFTKQNISSLVSVFWDDQ 60
QY 61 ENLVNEVYLGEKEDSVHSKYMGRTSFDSWTLRLHNLQIKDKGLYQCIHHKKPTGM 120
Db 61 QKLVLYEHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNLQIKDMGSYDCFIQKKPPTGS 120
QY 121 IRIHMNSLSVLANSFQPEIVPISNITENVYINLTCSIHGYPEPKMVSLLRTKNSTI 180
Db 121 IILQOTLTELAVANFSEPEIKLDQNVTCNSGINLTCMSKQGHKPKMYFLI--TNSTN 178
QY 181 EYDGMQKSDNVYDVSISLVSFPDVTSTNTIFCILETDKTRLLSPFSIELEDPQ 240
Db 179 EYGDNMQISQDNVTFLFSISNLSLSPFDGVVHMTVVCVLETESMKISSKPLNFTQEPFS 238
QY 241 PPPDHIPW--ITAVLPTVIICVMVFCILWLKWKXKXPRNSYKCGTNTWEREESQTKKR 298
Db 239 A---QTYWKEITASVTVALLLVWL--LIIVCHKKPNQPSRP---SNTASKLERSNADR 289
QY 299 EKIHIPE 305
Db 290 ETINLKE 296

RESULT 14
Q61238 PRELIMINARY; PRT; 314 AA.
AC Q61238;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE B7-2 protein.
GN CD86 OR B7-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=96094437; PubMed=7499829;
RA Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;
RT "Differential expression of alternate mb7-2 transcripts.";
RL J. Immunol. 155:5490-5497(1995).
DR EMBL; U39456; AAC52335.1; -.
DR EMBL; U39460; AAC52335.1; JOINED.
DR EMBL; U39461; AAC52335.1; JOINED.
DR EMBL; U39462; AAC52335.1; JOINED.
DR EMBL; U39463; AAC52335.1; JOINED.
DR EMBL; U39464; AAC52335.1; JOINED.
DR EMBL; U39465; AAC52335.1; JOINED.
DR EMBL; U39466; AAC52335.1; JOINED.
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 11:23:14 ; Search time 34.5502 Seconds
(without alignments)
1268.864 Million cell updates/sec

Title: US-09-425-516-2

Perfect score: 1733

Sequence: 1 MDPQCTGLSNILFVNAFL.....AQRVFKSKTSCDKSDTCF 329

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1733	100.0	329	16 AAR67984	Human B lymphocyte
2	1733	100.0	329	18 AAW08467	Human B lymphocyte
3	1733	100.0	329	20 AAW73638	Human B7-2 antigen
4	1733	100.0	329	21 AAB37085	Human B lymphocyte
5	1733	100.0	329	23 AAE14634	Human B7-2 protein
6	1696	97.9	323	16 AAR71478	B70 type B antigen
7	1696	97.9	323	21 AAY44290	Human B7.2 co-stim
8	1696	97.9	323	23 AAE15830	Human co-stimulato
9	1282	74.0	260	19 AAW42339	CD86 extracellular
10	1252	72.2	246	20 AAW86005	Human B7-2 extrac

11	1252	72.2	246	22 AAB83837	Amino acid sequenc
12	1241	71.6	244	20 AAW90209	hb7.1his soluble f
13	1241	71.6	477	20 AAW90207	hb7.2Fc soluble fu
14	1003	57.9	329	20 AAY41076	Canine B7-2 protei
15	991	57.2	250	18 AAM14944	Chimeric human/po
16	953	55.0	325	21 AAY95324	Human costimulator
17	950	54.8	325	21 AAY95321	Pig costimulator
18	912	52.6	332	20 AAY41079	Feline B7-2 protei
19	903	52.1	329	21 AAY32285	Feline CD86 (B7-2)
20	903	52.1	329	21 AAY32278	Cat CD86 (B7-2) li
21	903	52.1	329	23 AA017734	Feline CD86 Feli
22	903	52.1	329	23 AAU78121	Feline CD86 protei
23	886.5	51.2	280	20 AAY41078	Canine B7-2S prote
24	744.5	43.0	309	16 AAR67988	Murine B lymphocy
25	743.5	42.9	309	18 AAW08468	Mouse B lymphocy
26	743.5	42.9	309	20 AAW73639	Mouse B7-2 antigen
27	743.5	42.9	309	21 AAB37086	Mouse B lymphocy
28	724.5	41.8	314	16 AAR82899	Mouse B7-2 alterna
29	702.5	40.5	313	19 AAW34452	Rat CD86 Rattus
30	650.5	37.5	358	21 AAY44414	B7.2-beta 2 microg
31	636	36.7	339	21 AAY44413	B7.2-beta 2 microg
32	577	33.3	110	18 AAW08472	Human B lymphocy
33	577	33.3	110	21 AAB37092	Human B7-2 variabl
34	533	30.8	102	21 AAG00421	Human secreted pro
35	517	29.8	102	18 AAW08473	Human B lymphocy
36	517	29.8	102	21 AAB37093	Human B7-2 constan
37	365.5	21.1	169	20 AAY41080	Feline B7-2 protei
38	328	18.9	61	16 AAR82891	Human B7-2 cytopla
39	271.5	15.7	119	20 AAY41081	Feline B7-2 protei
40	250	14.4	306	16 AAR67990	Murine B lymphocy
41	247	14.3	306	16 AAR82893	Mouse B7-1 alterna
42	245.5	14.2	320	16 AAR82892	Mouse B7-1 alterna
43	244	14.1	306	22 AAB19960	Mouse B lymphocy
44	244	14.1	306	23 AAU99783	T-cell costimulati
45	244	14.1	306	23 AAM50796	Mouse B-lymphocyte

ALIGNMENTS

RESULT 1
AAR67984
ID AAR67984 standard; Protein; 329 AA.
XX AC AAR67984;
XX DT 20-AUG-1995 (first entry)
DE Human B lymphocyte antigen B7-2 predicted from clone 29.
KW CTLA4/CD28; counter receptor; B lymphocyte antigen; B7-2.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= secretory signal peptide
FT Domain 24..245
FT /label= extracellular Ig superfamily,V-& C-like
FT /note= "claimed"
FT Domain 246..268
FT /label= hydrophobic transmembrane domain
FT Domain 269..329
FT /label= cytoplasmic domain
FT Domain 40..110
FT /label= Ig-like domain
FT Domain 157..218
FT /label= Ig-like domain
FT Region 81..89
FT /label= CTLA4 or CD28 binding sequence
FT Region 188-200
FT /label= CTLA4 or CD28 binding sequence
FT Domain 269-282

FT	/note= "probably involved in intracellular signalling"	
FT		
XX		
FN	WO9503408-A.	
XX		
PD	02-FEB-1995.	
XX		
PF	26-JUL-1994; 94WO-US08423.	
XX		
PR	26-JUL-1993; 93US-0101624.	
PR	19-AUG-1993; 93US-0109393.	
PR	03-NOV-1993; 93US-0147773.	
XX		
XX	(DAND) DANA FARBEN CANCER INST INC.	
PA	(REPK) REPLIGEN CORP.	
XX		
PI	Freeman GJ, Gray GS, Greenfield E, Nadler LM;	
XX		
XX	WPI; 1995-075236/10.	
DR	N-PSDB; AAQ81351.	
DR		
XX		
PT	Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful	
FT	for enhancing or suppressing T-cell mediated immune responses	
XX		
PS	Claim 35; Fig 8; 175pp; English.	
XX		
CC	A cDNA library was constructed in the pCDM8 vector using poly A+ RNA	
CC	from the human anti-IgM activated B cells. Four clones were strongly	
CC	positive for B7-2 expression by indirect immunofluorescence using	
CC	CTLA4lg and flow cytometric analysis. The B7-2 cDNA insert in clone	
CC	29 was sequenced in the pCDM8 expression vector employing the	
CC	following strategy. Initial sequencing was performed using	
CC	sequencing primers T7 (AAQ81352), CDM8R (AAQ81353) (Invitrogen)	
CC	homologous to pCDM8 vector sequences adjacent to the clone B7-2 cDNA.	
CC	Sequencing was performed using dye terminator chemistry and an ABI	
CC	automated DNA sequencer. DNA sequence obtained using these primers was used	
CC	to design additional sequencing primers (see AAQ81354-881363). This cycle	
CC	of sequencing and selection of additional primers was continued until	
CC	the B7-2 cDNA was completely sequenced on both strands. The human	
CC	B7-2 clone 29 cDNA sequence is given in AAQ81351. The predicted	
CC	protein sequence (AAQ81358) exhibits many features common to other	
CC	type 1 Ig superfamily membrane proteins. Following cleavage of the	
CC	signal peptide the resulting membrane-bound protein would have an	
CC	unmodified mol. wt. of approx. 34 kDa. The extracellular domain	
CC	contains eight potential N-linked glycosylation sites. E. coli	
CC	transfected with a vector contg. the cDNA insert of clone 29 was	
CC	deposited under ATCC 69357 on July 26 1993.	
XX		
SQ	Sequence 329 AA;	
Query Match 100.0%; Score 1733; DB 16; Length 329;		
Best Local Similarity 100.0%; Pred. No. 8.3e-151;		
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 MDPQCTMGUSNTLFWAFLLSGAAPLKIQAYFNETADLPQFANSQNSLSLVWFQDQ 60	
Db	1 MDPQCTMGUSNTLFWAFLLSGAAPLKIQAYFNETADLPQFANSQNSLSLVWFQDQ 60	
Qy	61 ENLVNEVYLGEKFDSDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKPTGM 120	
Db	61 ENLVNEVYLGEKFDSDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKPTGM 120	
Qy	121 IRTHQNSLSVLNFSQPEIVPISNTENYINLTCSGSIHGYPEPKKMSVLLRTKNSTI 180	
Db	121 IRTHQNSLSVLNFSQPEIVPISNTENYINLTCSGSIHGYPEPKKMSVLLRTKNSTI 180	
Qy	181 EYDGINQSDQNVNTELYDVSTLSVSPDPVTSNMTIFCILETDKTRLLSPFIELEDQ 240	
Db	181 EYDGINQSDQNVNTELYDVSTLSVSPDPVTSNMTIFCILETDKTRLLSPFIELEDQ 240	
Qy	241 PPPDHIPWITAVLPTVIICVMVFCLILWKWKKKRPRNSYKCGTNTWERESEQTKKREK 300	
Db	241 PPPDHIPWITAVLPTVIICVMVFCLILWKWKKKRPRNSYKCGTNTWERESEQTKKREK 300	

Qy 301 IHIPERSDEAQRVFKSKTSKSDKSDTCF 329
|||||
Db 301 IHIPERSDEAQRVFKSKTSKSDKSDTCF 329

RESULT 2
AAW08467
ID AAW08467 standard; Protein: 329 AA.
XX
AC AAW08467;
XX
DT 08-APR-1997 (first entry)
XX
DE Human B lymphocyte antigen B7-2.
XX
KW CTLA4; CD28; ligand; B7-2; B lymphocyte antigen; B-cell;
KW costimulation; immunoglobulin; antibody; autoimmune disease;
KW allergy; tumour; vaccine; graft versus host disease; T-cell;
KW T lymphocyte; TH2 response; immunosuppressive; immunostimulant;
KW therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..13
FT /label= Sig_peptide
FT Protein 24..329
FT /label= Mat_protein
FT Domain 24..245
FT /label= Extracellular domain
FT /note= "extracellular Ig superfamily V and C-like domain"
FT Region 40..110
FT /label= Ig-like_domain
FT Region 157..218
FT /label= Ig-like_domain
FT Binding-site 81..89
FT label= CTLA4/CD28_binding_site
FT Binding-site 188..200
FT label= CTLA4/CD28_binding_site
FT Region 24..133
FT /label= Variable_region
FT /note= "(Claim 42)"
FT Region 134..235
FT /label= Constant_region
FT Domain 246..268
FT /label= Transmembrane_domain
FT Domain 269..329
FT /label= Cytoplasmic_domain
FT Region 268..282
FT /note= "region probably involved in intracellular signalling"
FT Modified-site 33
FT /label= Glycosylation
FT /note= "putative N-glycosylation site"
FT Modified-site 47
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FT Modified-site 146
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FT /label= Glycosylation

FT /note= "putative N-glycosylation site"

XX WO9640915-A2.
XX 19-DEC-1996.
XX 06-JUN-1996; 96WO-US09052.
XX 07-JUN-1995; 95US-0479744.
XX (DAND) DANA FARBER CANCER INST INC.
XX (REPK) REPLIGEN CORP.
XX Freeman GJ, Gray GS, Nadler LM;
XX WPI; 1997-077269/07.
XX N-PSDB; AAT49181.
XX DNA encoding a B7-2 fusion protein - used to enhance or down
XX regulate B lymphocyte antigens
XX Claim 4; Page 95-96; 171pp; English.
XX Human B-lymphocyte antigen B7-2 (AAW08467) is a CTLA4/CD28 ligand
XX which costimulates T cell activation. It shows 26% amino acid
XX identity to human B7-1. Its sequence was deduced from a cDNA
XX clone (AAT49181) isolated from an anti-ICM activated B cell cDNA
XX library. Novel fusion proteins comprising the extracellular domain,
XX variable region-like or constant region-like domains of B7-2 (see
XX also AAW08472-73) and e.g. an immunoglobulin heavy chain constant
XX region can be expressed in host cells and used to enhance or
XX suppress T cell-mediated immune responses.
XX SQ Sequence 329 AA;

Query Match 100.0%; Score 1733; DB 18; Length 329;
Best Local Similarity 100.0%; Pred. No. 8.3e-151;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDPOCTMGLSNILFVMAFLLSGAAPLKIQAIFNETADLPCQFANSONQSLSELVVFWDQ 60
Db 1 MDPOCTMGLSNILFVMAFLLSGAAPLKIQAIFNETADLPCQFANSONQSLSELVVFWDQ 60
Qy 61 ENLVNEVYLGEKEFDSVHSKYMGRTSFSDSWTLRLHNLQIKDGLYQCIHHKKPTGM 120
Db 61 ENLVNEVYLGEKEFDSVHSKYMGRTSFSDSWTLRLHNLQIKDGLYQCIHHKKPTGM 120
Qy 121 IRIHOMNSELSVLANFSQPEIPIISNITENVYINLTCSHGYPEPKMSVLLRTKNSTI 180
Db 121 IRIHOMNSELSVLANFSQPEIPIISNITENVYINLTCSHGYPEPKMSVLLRTKNSTI 180
Qy 181 EYDGIOMKSDQNVTELYDVSISLSVSPDPVTSNMIFCILETDKTRLLSSPFSIELED 240
Db 181 EYDGIOMKSDQNVTELYDVSISLSVSPDPVTSNMIFCILETDKTRLLSSPFSIELED 240
Qy 241 PPDHPIPWITAVLPTVIIICVMVFCILILWKWKKKRPNYSKCGTNTMEREESEQTKREK 300
Db 241 PPDHPIPWITAVLPTVIIICVMVFCILILWKWKKKRPNYSKCGTNTMEREESEQTKREK 300
Qy 301 IHIPERSDEAQRVFKSKTSKSDSDTCF 329
Db 301 IHIPERSDEAQRVFKSKTSKSDSDTCF 329

RESULT 3
AAW73638
ID AAW73638 standard; Protein; 329 AA.
XX AAW73638;
XX AC AAW73638;
XX DT 23-MAR-1999 (first entry)
XX DE Human B7-2 antigen.

XX B7-2 antigen; mammalian tumour cell; T cell costimulation; CD28 ligand;
XX CTLA4 ligand; therapy; T-cell response; human.
XX OS Homo sapiens.
XX US5861310-A.
XX 19-JAN-1999.
XX 30-MAY-1995; 95US-0456104.
XX 30-MAY-1995; 95US-0456104.
XX 03-NOV-1993; 93US-0147773.
XX (DAND) DANA FARBER CANCER INST INC.
XX Freeman GJ, Gray GS, Nadler LM;
XX WPI; 1999-130394/11.
XX N-PSDB; AAV55784.
XX Tumour cell transfected to express B7-2 molecule - useful for tumour
XX therapy by stimulating T-cell response
XX Claim 10; Column 27-30; 27pp; English.
XX This sequence is the human B7-2 antigen, which can be used in the
XX method of the invention. The method is for transfecting an isolated
XX mammalian tumour cell with an exogenous nucleic acid molecule encoding a
XX mammalian B7-2 molecule, where the B7-2 molecule is expressed in the
XX tumour cell is capable of costimulating a T cell and is capable of
XX binding a CD28 or CTLA4 ligand. The method is useful for treating tumours
XX by stimulating a T-cell response against tumour cells in vivo.
XX SQ Sequence 329 AA;

Query Match 100.0%; Score 1733; DB 20; Length 329;
Best Local Similarity 100.0%; Pred. No. 8.3e-151;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDPOCTMGLSNILFVMAFLLSGAAPLKIQAIFNETADLPCQFANSONQSLSELVVFWDQ 60
Db 1 MDPOCTMGLSNILFVMAFLLSGAAPLKIQAIFNETADLPCQFANSONQSLSELVVFWDQ 60
Qy 61 ENLVNEVYLGEKEFDSVHSKYMGRTSFSDSWTLRLHNLQIKDGLYQCIHHKKPTGM 120
Db 61 ENLVNEVYLGEKEFDSVHSKYMGRTSFSDSWTLRLHNLQIKDGLYQCIHHKKPTGM 120
Qy 121 IRIHOMNSELSVLANFSQPEIPIISNITENVYINLTCSHGYPEPKMSVLLRTKNSTI 180
Db 121 IRIHOMNSELSVLANFSQPEIPIISNITENVYINLTCSHGYPEPKMSVLLRTKNSTI 180
Qy 181 EYDGIOMKSDQNVTELYDVSISLSVSPDPVTSNMIFCILETDKTRLLSSPFSIELED 240
Db 181 EYDGIOMKSDQNVTELYDVSISLSVSPDPVTSNMIFCILETDKTRLLSSPFSIELED 240
Qy 241 PPDHPIPWITAVLPTVIIICVMVFCILILWKWKKKRPNYSKCGTNTMEREESEQTKREK 300
Db 241 PPDHPIPWITAVLPTVIIICVMVFCILILWKWKKKRPNYSKCGTNTMEREESEQTKREK 300
Qy 301 IHIPERSDEAQRVFKSKTSKSDSDTCF 329
Db 301 IHIPERSDEAQRVFKSKTSKSDSDTCF 329

RESULT 4
AAB37085
ID AAB37085 standard; Protein; 329 AA.
XX AAB37085;
XX AC AAB37085;
XX DT 28-MAR-2001 (first entry)

XX DE Human B lymphocyte antigen B7-2 from clone 29.

XX KW Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;

XX KW antigen; extracellular domain; CTLA4; immunoglobulin constant region;

XX KW immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage;

XX KW T cell-mediated immune response; transplantation; vaccination.

XX OS Homo sapiens.

XX PN US6130316-A.

XX PD 10-OCT-2000.

XX PF 26-JUL-1994; 94US-0280757.

XX PR 26-JUL-1993; 93US-0101624.

XX PR 19-AUG-1993; 93US-0109393.

XX PR 03-NOV-1993; 93US-0147733.

XX (DAND) DANA FARBER CANCER INST INC.

XX (REPK) REPLIGEN CORP.

XX Freeman GJ, Nadler LM, Gray GS, Greenfield E;

XX WPI; 2000-655681/63.

XX N-PSDB; AAC84049.

XX Nucleic acids and fusion proteins of CTLA4/CD28 ligands, useful for

XX enhancing or suppressing T cell-mediated immune responses, especially

XX during tissue, skin or organ transplantation, or in graft-versus-host

XX disease -

XX Claim 23; Fig 8; 83pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a

XX fusion protein comprising a first nucleotide sequence encoding a first

XX peptide, and a second nucleotide sequence encoding a second peptide.

XX The first nucleotide sequence hybridizes in 6 X sodium chloride/sodium

XX citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C

XX to a portion of a nucleotide sequence which encodes a human or murine

XX B lymphocyte antigen (B7-2) extracellular domain. The first peptide has

XX the ability to bind CD28 or CTLA4. The first peptide has an amino acid

XX sequence that is identical or at least 50% identical with the

XX extracellular domain of a human B7-2 peptide (AAB37085). The second

XX peptide is especially an immunoglobulin constant region. This sequence

XX represents the human B lymphocyte antigen B7-2 encoded by the human B7-2

XX clone 29 cDNA. The nucleic acid is used as a first sequence in the

XX construct of the invention. The nucleic acid are useful in various

XX expression vectors to direct synthesis of the corresponding proteins or

XX peptides in a variety of hosts, particularly eukaryotic cells, e.g.

XX mammalian or insect cell culture. The nucleic acids are also useful for

XX enhancing the immunogenicity of a mammalian cell, e.g. tumour cell

XX (sarcoma) or an antigen presenting cell (macrophage). The fusion proteins

XX or peptides are useful for enhancing or suppressing T cell-mediated

XX immune responses, e.g. in situations of tissue, skin or organ

XX transplantation, or in graft-versus-host disease. The proteins are also

XX useful for enhancing the efficacy of vaccination against a variety of

XX pathogens, and may also be used to upregulate an immune response against

XX a particular pathogen during an infection or against a tumour in a

XX tumour-bearing host.

XX Sequence 329 AA;

Query Match 100.0%; Score 1733; DB 21; Length 329;

Best Local Similarity 100.0%; Pred. No. 8.3e-151;

Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPOCTMGLSNILFVMAFLSGLAFLKIQAYFNETADLPQCFANSONSLSELYVFWQDQ 60

DB 1 MDPOCTMGLSNILFVMAFLSGLAFLKIQAYFNETADLPQCFANSONSLSELYVFWQDQ 60

QY 61 ENLVNLEVYLKGEKFDVSHSKYMGRTSFDSDSWTLRLHLNLQIKDKGLYQCIIHHKXPTGM 120

Db 61 ENLVNLEVYLKGEKFDVSHSKYMGRTSFDSDSWTLRLHLNLQIKDKGLYQCIIHHKXPTGM 120

QY 121 IRIHOMNSELVLANFSPQPEIVPISNITENVYINLTCSSIHGYPPKMSVLLRTKNSTI 180

Db 121 IRIHOMNSELVLANFSPQPEIVPISNITENVYINLTCSSIHGYPPKMSVLLRTKNSTI 180

QY 181 EYDGIQKSDQNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPQ 240

Db 181 EYDGIQKSDQNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPQ 240

QY 241 PPDHPITAVITAVLPVILCVWVFCILWKWKKKRPRNSYKCGTNTMEREESEQTKKREK 300

Db 241 PPDHPITAVITAVLPVILCVWVFCILWKWKKKRPRNSYKCGTNTMEREESEQTKKREK 300

QY 301 IHIPERSDEAQRVFKSSKTSKCDKSDTCF 329

Db 301 IHIPERSDEAQRVFKSSKTSKCDKSDTCF 329

RESULT 5

AAE14634

ID AAE14634 standard; Protein; 329 AA.

XX AC AAE14634;

XX DT 16-JUL-2002 (first entry)

XX DE Human B7-2 protein.

XX T cell; CD3; accessory molecule; CD28; cancer; infectious disease;

XX immunotherapy; human immunodeficiency virus; HIV infection;

XX cytokine; human; B7-2; CD86.

XX Homo sapiens.

XX US6352694-B1.

XX 05-MAR-2002.

XX 10-MAR-1995; 95US-0403253.

XX 03-JUN-1994; 94US-0253964.

XX (GEMY) GENETICS INST INC.

XX (UNWI) UNIV MICHIGAN.

XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2002-314696/35.

XX N-PSDB; AAD27968.

XX Inducing T cell population to proliferate, useful in cancer therapy,

XX comprises activating T cells by contacting T cells in vitro with

XX immobilised anti-CD3 antibody and stimulating accessory molecule on T

XX cell surface -

XX Example 11; Column 63-66; 71pp; English.

XX The invention relates to a method of inducing T cell population to

XX proliferate for use in therapy comprising activating T cells by

XX contacting T cells in vitro with anti-CD3 antibody which is immobilised

XX on solid phase surface, and stimulating accessory molecule on T cell

XX surface in vitro with anti-CD28 antibody, or stimulatory form of

XX natural ligand for CD28 such as B7-1 or B7-2. The method is useful

XX for inducing a population of T cells to proliferate in sufficient

XX numbers for use in therapy e.g., for treating cancer or an infectious

XX disease. The method can be used to selectively expand the

XX population of CD28⁺, CD4⁺, CD8⁺, CD28RA⁺ or CD28RO⁺ T cells for

XX immunotherapy. The T cell population resulting by the method can be

XX genetically transduced and used for immunotherapy or can be used for in

XX vitro analysis of infectious agents such as human immunodeficiency

XX virus (HIV). Proliferation of a population of CD4⁺ T cells obtained

CC from an individual infected with HIV can be achieved and the cells
 CC referred resistant to HIV infection. Following the expansion of the T
 CC cells to sufficient numbers, the expanded T cells are restored to the
 CC individual. Also CD4+ T cells expanded by the above mentioned is
 CC useful for treating HIV infection in an individual. A population
 CC of tumour-infiltrating lymphocytes can be obtained from an individual
 CC afflicted with cancer and the T cells stimulated to proliferate to
 CC sufficient numbers and restored to the individual. The supernatants from
 CC cultures of T cells expanded from above mentioned method are useful as a
 CC rich source of cytokines and can be used to sustain T cells in vivo or
 CC ex vivo. Stimulating and expanding a population of antigen specific
 CC T cells are useful in therapeutic conditions where it is desirable to
 CC upregulate an immune response. The T cell proliferation occurs in
 CC the absence of exogenous growth factors or accessory cells. The present
 CC sequence is human B7-2 (CD86) protein used in the invention.

XX
 SQ Sequence 329 AA;

Query Match 100.0%; Score 1733; DB 23; Length 329;
 Best Local Similarity 100.0%; Pred. No. 8.3e-151; Indels 0; Gaps 0;
 Matches 329; Conservative 0; Mismatches 0;

Qy 1 MDPQCTMGLSNILFVMAFLLSGAAPLKIQAIFYNETADLPCQFANSQNSLSLVFWQDQ 60
 Db 1 MDPQCTMGLSNILFVMAFLLSGAAPLKIQAIFYNETADLPCQFANSQNSLSLVFWQDQ 60

Qy 61 ENLVNVEVYLGKEKFDPSVHVKYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGM 120
 Db 61 ENLVNVEVYLGKEKFDPSVHVKYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGM 120

Qy 121 IRIHQNSLSVLANFSQPEIVPISNITENVYINLTCSIIHGYPEPKMSVLLRTKNSTI 180
 Db 121 IRIHQNSLSVLANFSQPEIVPISNITENVYINLTCSIIHGYPEPKMSVLLRTKNSTI 180

Qy 181 EYDGMQKSDNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPO 240
 Db 181 EYDGMQKSDNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPO 240

Qy 241 PPPDHIPWITAVLPTVVIICVMVFCILILWKWKKKRPNRSYKCGTNTMERESSEQTKKREK 300
 Db 241 PPPDHIPWITAVLPTVVIICVMVFCILILWKWKKKRPNRSYKCGTNTMERESSEQTKKREK 300

Qy 301 IHIPEKSDAQRVFKSSKTSCKSDTCF 329
 Db 301 IHIPEKSDAQRVFKSSKTSCKSDTCF 329

RESULT 6
 AAR71478
 ID AAR71478 standard; Protein; 323 AA.
 AC AAR71478;
 XX
 XX 09-OCT-1995 (first entry)
 DT
 XX
 XX B70 type B antigen which binds CTLA-4 and CD28.
 DE
 XX
 XX B70 antigen; CTLA-4; CD28; T cell response.
 KW
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO9506738-A.
 FN
 XX
 XX 09-MAR-1995.
 PD
 XX
 XX 02-SEP-1994; 94WO-US09642.
 PF
 XX
 XX 03-SEP-1993; 93US-0116882.
 PR
 XX
 XX 13-SEP-1993; 93US-0120606.
 ER
 XX
 XX (AZUM/) AZUMA M.
 PA (OKUM/) OKUMURA K.
 PA (SCHE) SCHERING CORP.

XX Azuma M, Lanier LL, Okumura K, Phillips JH;
 PI Somoza Diaz-sarmiento M;
 XX WPI; 1995-115453/15.
 DR N-PSDB; AAQ85873.
 XX
 XX New CTLA-4/CD28 binding protein, B70 - used to develop prods for
 PT modulating the physiology, growth or development of cells.
 PS
 XX Claim 3; Page 44-45; 55pp; English.
 XX
 CC B70 is a natural proteinaceous binding partner for CTLA-4 and CD28
 CC markers/antigens. It is distinct from the known B7/BBI marker. It is
 CC representative of 'type B' markers/antigens/binding partners. The
 CC type A markers/binding partners include both CTLA-4 and CD28 and
 CC antibodies specific for B70, and are characterised, in part, by the
 CC property of serving as a binding partner for B70. A cDNA encoding a
 CC B70 antigen was cloned by expression cloning using mAb IT2.236 to
 CC select COS7 cells transfected with a cDNA library cloned into the
 CC pUPE14 vector. The library was made from RNA isolated from a human
 CC EBV-transformed B-lymphoblastoid cell line JY.
 XX
 SQ Sequence 323 AA;

Query Match 97.9%; Score 1696; DB 16; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2e-147;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MGLSNILFVMAFLLSGAAPLKIQAIFYNETADLPCQFANSQNSLSLVFWQDQENLVN 66
 Db 1 MGLSNILFVMAFLLSGAAPLKIQAIFYNETADLPCQFANSQNSLSLVFWQDQENLVN 60

Qy 67 EYVLGKEKFDPSVHVKYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGMIRIHM 126
 Db 61 EYVLGKEKFDPSVHVKYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGMIRIHM 120

Qy 127 NSELSVLANFSQPEIVPISNITENVYINLTCSIIHGYPEPKMSVLLRTKNSTIEYDGM 186
 Db 121 NSELSVLANFSQPEIVPISNITENVYINLTCSIIHGYPEPKMSVLLRTKNSTIEYDGM 180

Qy 187 QKSDQNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPOPPDHI 246
 Db 181 QKSDQNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPOPPDHI 240

Qy 247 PWITAVLPTVVIICVMVFCILILWKWKKKRPNRSYKCGTNTMERESSEQTKKREKIHIPER 306
 Db 241 PWITAVLPTVVIICVMVFCILILWKWKKKRPNRSYKCGTNTMERESSEQTKKREKIHIPER 300

Qy 307 SDEAQRVFKSSKTSCKSDTCF 329
 Db 301 SDEAQRVFKSSKTSCKSDTCF 323

RESULT 7
 AAY44290
 ID AAY44290 standard; Protein; 323 AA.
 XX
 XX AAY44290;
 AC
 XX
 XX 29-FEB-2000 (first entry)
 DT
 XX
 XX Human B7.2 co-stimulatory molecule.
 DE
 XX
 XX Human B7.2 co-stimulatory molecule; antigen presenting cell;
 KW immune response; cell surface receptor; Major histocompatibility complex;
 KW MHC classII; proton motor force; mitochondrial membrane potential;
 KW mitochondrial metabolism; cancer; autoimmune disease; glycoprotein;
 KW neurodegenerative disorder.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO953953-A2.
 PN

```
XX PD 28-OCT-1999.
XX PF 30-MAR-1999; 99WO-US06874.
XX PR 17-APR-1998; 98US-0082250.
XX PR 29-JUL-1998; 98US-0094519.
XX PR 24-SEP-1998; 98US-0101580.
XX PA (UYVE-) UNIV VERMONT.
XX PI Newell MK;
XX DR WPI; 2000-096773/08.
XX DR N-PSDB; AA229321.
XX PT Use of cell surface and membrane characteristics for developing
XX PT products for treating cancers, autoimmune diseases or neurodegenerative
XX PT diseases -
XX PS Disclosure; Page 116-117; 123pp; English.
XX CC The present sequence is human B7.2 co-stimulatory molecule. This is
XX CC a glycoprotein on the surface of antigen presenting cells. This is
XX CC involved in stimulation of an immune response by its ability to interact
XX CC with various immune cell surface receptors. The regulation of cell
XX CC surface expression of MHC classII and co-stimulatory molecule B7 can be
XX CC manipulated by regulating the intracellular dissipation of proton motor
XX CC force which can be assessed in terms of mitochondrial membrane potential.
XX CC these methods can be used for regulating cell growth and division to
XX CC control disease processes by manipulating mitochondrial metabolism and
XX CC the expression of cell surface immune proteins. They can be used for
XX CC treating diseases associated with excessive cellular division, aberrant
XX CC differentiation, and premature cellular death, e.g. cancers, autoimmune
XX CC diseases, neurodegenerative disorders etc.
XX SQ Sequence 323 AA;
Query Match 97.9%; Score 1696; DB 21; Length 323;
Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MGLSNILFWMAFLLSGAAPLKIQAIFNETADLPCQFANSQNSLSLVFWQDENLVN 66
DB 1 MGLSNILFWMAFLLSGAAPLKIQAIFNETADLPCQFANSQNSLSLVFWQDENLVN 60
QY 67 EYVLGKEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKPTGMIRIHO 126
DB 61 EYVLGKEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKPTGMIRIHO 120
QY 127 NSELSVLANFSPQEIPIVPSINITENVYINLTCSIIHGYPEPKMSVLLRTKNSTIYDGM 186
DB 121 NSELSVLANFSPQEIPIVPSINITENVYINLTCSIIHGYPEPKMSVLLRTKNSTIYDGM 180
QY 187 QKSQDNVTELYDVSISLSVSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDPOPPDHI 246
DB 181 QKSQDNVTELYDVSISLSVSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDPOPPDHI 240
QY 247 PWITAVLPTVILCVWVFCLILWKWKKKRPRNSYKCGTNTWEREESQTKREKIHIPER 306
DB 241 PWITAVLPTVILCVWVFCLILWKWKKKRPRNSYKCGTNTWEREESQTKREKIHIPER 300
QY 307 SDEAQRVFKSKTSCKSDTCF 329
DB 301 SDEAQRVFKSKTSCKSDTCF 323
RESULT 8
AAE15830
ID AAE15830 standard; Protein; 323 AA.
XX AC AAE15830;
XX XX
```

```
DT 26-MAR-2002 (first entry)
XX Human co-stimulatory molecule, B7-2 protein.
DE Human, vaccine; immunostimulatory molecule; interferon; IFN; therapy;
XX antigen presentation; vaccine; tumorigenesis; cancer; cytostatic;
KW antitumor; antibacterial; virucide; fungicide; protozoacide; B7-2.
XX OS Homo sapiens.
XX WO2001188097-A1.
XX PD 22-NOV-2001.
XX PF 17-MAY-2001; 2001WO-AU00565.
XX PR 17-MAY-2000; 2000AU-0007553.
XX PA (MONU ) UNIV MONASH.
XX PI Ralph SJ;
XX DR WPI; 2002-082990/11.
XX DR N-PSDB; AAD25510.
XX PT New composition, useful for treatment and/or prophylaxis of cancer and
XX PT tumor, comprises immunostimulatory molecule and animal cells cultured
XX PT in presence of interferon to enhance antigen presenting function of the
XX PT cells -
XX PS Claim 8; Page 102-103; 127pp; English.
XX CC The present invention relates to a composition of matter comprising an
XX CC immunostimulatory molecule and animal cells cultured in the presence of
XX CC at least one interferon (IFN) for a time and under conditions sufficient
XX CC to enhance the antigen presenting function of the cells. The invention
XX CC is used as vaccine. The composition is useful for treatment and/or
XX CC prophylaxis of tumorigenesis, cancer, viral, bacterial, fungal and
XX CC protozoal infections. The composition which comprises the soluble
XX CC immunostimulatory molecule and the cultured animal cells is administered
XX CC separately, sequentially or simultaneously to the patient. The present
XX CC sequence is human co-stimulatory molecule, B7-2 protein.
XX SQ Sequence 323 AA;
Query Match 97.9%; Score 1696; DB 23; Length 323;
Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MGLSNILFWMAFLLSGAAPLKIQAIFNETADLPCQFANSQNSLSLVFWQDENLVN 66
DB 1 MGLSNILFWMAFLLSGAAPLKIQAIFNETADLPCQFANSQNSLSLVFWQDENLVN 60
QY 67 EYVLGKEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKPTGMIRIHO 126
DB 61 EYVLGKEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKPTGMIRIHO 120
QY 127 NSELSVLANFSPQEIPIVPSINITENVYINLTCSIIHGYPEPKMSVLLRTKNSTIYDGM 186
DB 121 NSELSVLANFSPQEIPIVPSINITENVYINLTCSIIHGYPEPKMSVLLRTKNSTIYDGM 180
QY 187 QKSQDNVTELYDVSISLSVSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDPOPPDHI 246
DB 181 QKSQDNVTELYDVSISLSVSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDPOPPDHI 240
QY 247 PWITAVLPTVILCVWVFCLILWKWKKKRPRNSYKCGTNTWEREESQTKREKIHIPER 306
DB 241 PWITAVLPTVILCVWVFCLILWKWKKKRPRNSYKCGTNTWEREESQTKREKIHIPER 300
QY 307 SDEAQRVFKSKTSCKSDTCF 329
DB 301 SDEAQRVFKSKTSCKSDTCF 323
```

RESULT 9
 AAW42339
 ID AAW42339 standard; Protein; 260 AA.
 AC AAW42339;
 XX
 DT 22-JUN-1998 (first entry)
 DE CD86 extracellular domain.
 XX
 KW Hexameric fusion protein; IgA; alpha-tp; tailpiece; antibody;
 KW CD86; CD28; CTLA-4; vaccine; diagnosis; binding assay; screening;
 KW human, ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= Sig-peptide
 FT Protein 26..260
 FT /label= Mat_protein
 FT Peptide 245..250
 FT /label= Ig_hinge
 XX
 PN MO9747732-A2.
 PD 18-DEC-1997.
 XX
 PF 13-JUN-1997; 97WO-US12599.
 XX
 PR 21-FEB-1997; 97US-0038915.
 PR 14-JUN-1996; 96US-0019934.
 PR 19-FEB-1997; 97US-0043948.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Chaikin MA, Lyn SDP, Sweet RW, Truneh A;
 XX
 DR WPI; 1998-052299/05.
 DR N-PSDB; AAV03230.
 XX
 PT Hexameric fusion protein containing IgA antibody fragment - used for
 PT stimulating CD28 positive cells, or suppressing CTLA-4 positive
 PT cells
 XX
 PS Example 1; Fig 5A-B; 105pp; English.
 XX
 CC This protein comprises the signal region and extracellular
 CC domain of human CD86 encoded by a portion (see AAV03230) of
 CC plasmid CD86FcAlphatLink. This plasmid encodes a fusion protein
 CC comprising the CD86 signal peptide and extracellular domain
 CC grafted to a human IgG1 heavy chain Fc region and the tailpiece
 CC region (alpha-tp) (see AAW42344) of human IgA heavy chain. The
 CC processed fusion protein has been expressed as a hexamer in COS
 CC cells. The invention relates to novel hexameric fusion proteins
 CC comprising a dimeric binding protein such as CD86 provided at its
 CC C-terminus with a tailpiece that has the activity of alpha-tp. The
 CC tailpiece provides the fusion protein with the ability to form
 CC stable hexamers. Also claimed are polynucleotides encoding the
 CC hexameric fusion proteins, vectors, recombinant host cells and a
 CC method for producing the hexamers. The fusion protein is useful in
 CC therapeutics and vaccines, and is particularly well suited for
 CC applications for which the binding protein from which it is derived
 CC is unsatisfactory because of low binding affinity or for
 CC applications where multivalency is desired. Applications include
 CC diagnostics, binding assays and screening assays. CD86-Ig-alpha-tp
 CC fusion protein is used in claimed methods for stimulating CD28
 CC positive cells or suppressing CTLA-4 positive cells.
 XX
 SQ Sequence 260 AA;
 Query Match 74.0%; Score 1282; DB 19; Length 260;

Best Local Similarity 99.6%; Pred. No. 1.7e-109;
 Matches 246; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDPOCTMGLSNILFWAFLLSGAAPLKIQAVFNETADLPQOFANSQNSLSLWVFWQDQ 60
 DB 1 MDPOCTMGLSNILFWAFLLSGAAPLKIQAVFNETADLPQOFANSQNSLSLWVFWQDQ 60
 QY 61 ENLVNEVYLKGEKFSVHSKYMGRTSFDSDSWTLRLHNLIQDKGLYQCIHHKKPTGM 120
 DB 61 ENLVNEVYLKGEKFSVHSKYMGRTSFDSDSWTLRLHNLIQDKGLYQCIHHKKPTGM 120
 QY 121 IRIHOMSELVLANFSQPEIPIVINSITENYVINTCSSIHGYPEPKMSVLLRTKNSTI 180
 DB 121 IRIHOMSELVLANFSQPEIPIVINSITENYVINTCSSIHGYPEPKMSVLLRTKNSTI 180
 QY 181 EYDGIMQKSQDNVTELYDVISLSVSPFDVTSNMTIFCILETDKTRLLSPFSIELEDDQ 240
 DB 181 EYDGIMQKSQDNVTELYDVISLSVSPFDVTSNMTIFCILETDKTRLLSPFSIELEDDQ 240
 QY 241 PPPDHP 247
 DB 241 PPPDHP 247
 RESULT 10
 AAW86005
 ID AAW86005 standard; Protein; 246 AA.
 XX
 AC AAW86005;
 XX
 DT 15-MAR-1999 (first entry)
 DE Human B7-2 extracellular domain and linker.
 XX
 KW Tumour interacting protein; cancer; gene therapy; vector;
 KW 5T4 antigen; monoclonal antibody; single chain antibody;
 KW mouse; human; B7-2; co-stimulatory molecule.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..16
 FT /label= Sig_peptide
 FT Protein 17..241
 FT /label= Mat_protein
 FT /note= "B7-2 extracellular domain"
 FT Peptide 242..246
 FT /label= Linker
 XX
 PN WO9855607-A2.
 PD 10-DEC-1998.
 XX
 PF 04-JUN-1998; 98WO-GB01627.
 XX
 PR 04-JUL-1997; 97GB-0014230.
 PR 04-JUN-1997; 97GB-0011579.
 PR 20-JUN-1997; 97GB-0013150.
 XX
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 PI Bebbington CR, Carroll MW, Ellard FM, Kingsman SM;
 PI Myers KA;
 XX
 DR WPI; 1999-059910/05.
 DR N-PSDB; AAV80293.
 XX
 PT New vector encoding a tumour interacting protein for treating cancer
 PT - contains a desired nucleotide sequence and/or protein which
 PT recognises tumours, and is used as a gene delivery system to treat
 PT cancer
 XX

PS Example 5; Fig 4; 82pp; English.

XX This polypeptide comprises the extracellular domain (amino acids
CC 1-215) of human co-stimulatory molecule B7-2 joined to a C-terminal
CC flexible peptide linker. It is part of B7-2.5T4.1 co-stimulatory
CC domain, a fusion protein comprising the B7-2 extracellular domain
CC joined via the linker to an scFv (see AAW86002) derived from murine
CC 5T4 monoclonal antibody. B7-2.5T4.1 cDNA (see AAV80293) can be
CC inserted into vector PCI to allow expression of the fusion protein
CC in mammalian cells. The trophoblast cell surface antigen defined
CC by 5T4 is expressed at high levels on the cells of a wide variety
CC of human tumours. The invention relates to a vector comprising a
CC nucleotide sequence coding for a tumour interacting protein (TIP)
CC and optionally a nucleotide sequence of interest (NOI) which
CC encodes a protein of interest (POI), the vector being capable of
CC delivering the NOI and/or POI to the tumour recognised by the TIP.
CC Delivery can be in vivo or ex vivo. The vector is used to treat
CC cancer, and may also be used as a gene delivery system for
CC introducing at least 1 gene encoding a TIP (preferably a tumour
CC binding protein) into a haematopoietic cell lineage. B7-2 is
CC expected to bind specifically to CD28 and CTLA-4 present on human
CC T-cells.

XX SQ Sequence 246 AA;

Query Match 72.2%; Score 1252; DB 20; Length 246;
Best Local Similarity 100.0%; Pred. No. 9e-107;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGLSNILFVMAFLISGAAPLKIQAYFNETADLPQFANSQNSLSLVVFWQDQENLVN 66
DB 1 MGLSNILFVMAFLISGAAPLKIQAYFNETADLPQFANSQNSLSLVVFWQDQENLVN 60

QY 67 EYVLGKFKFDSVHSHKMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRIHO 126
DB 61 EYVLGKFKFDSVHSHKMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRIHO 120

QY 127 NSELSVLNFSQPEIPIVPSNITENVYINLTCSHIGYPKPKMSVLLRTKNSITIEDGIM 186
DB 121 NSELSVLNFSQPEIPIVPSNITENVYINLTCSHIGYPKPKMSVLLRTKNSITIEDGIM 180

QY 187 QKSDQNVTELYDVSISLSVSPDVTNNMTIFCILETDKTRLLSSPFSIELEDPQPPDHI 246
DB 181 QKSDQNVTELYDVSISLSVSPDVTNNMTIFCILETDKTRLLSSPFSIELEDPQPPDHI 240

QY 247 P 247
DB 241 P 241

RESULT 11
AAB83837
ID AAB83837 standard; Protein; 246 AA.
XX
AC AAB83837;
XX
XX Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
XX hypersensitivity; autoimmune disease; central nervous system disorder;
XX Parkinson's disease; periodontal disease; cardiopulmonary disease;
XX cardiovascular disease; gastrointestinal disorder; infection; diabetes;
XX Helicobacter-related disease; immune disorder.
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
PN WO200136486-A2.
XX
PD 25-MAY-2001.

DE Amino acid sequence of a B7-2.5T4.1 fusion protein.

XX

Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
XX hypersensitivity; autoimmune disease; central nervous system disorder;
XX Parkinson's disease; periodontal disease; cardiopulmonary disease;
XX cardiovascular disease; gastrointestinal disorder; infection; diabetes;
XX Helicobacter-related disease; immune disorder.
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
PN WO200136486-A2.
XX
PD 25-MAY-2001.

XX 13-NOV-2000; 2000WO-CB04317.
XX
XX 18-NOV-1999; 99WO-CB03859.
PR 15-FEB-2000; 2000GB-0003527.
PR 02-MAR-2000; 2000GB-0005071.
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
XX Kingman A, Kingman SM, Bebbington CR, Carroll MW, Ellard PM;
PI Myers KA;
XX WPI; 2001-343805/36.
DR N-PSDE; AAF89731.
XX
XX Use of single chain antibody capable of recognizing a disease
PT associated molecule for manufacturing a medicament for preventing
PT and/or treating a disease condition associated with disease associated
PT molecule -
XX
XX Example 3; Fig 4; 118pp; English.
XX
XX The specification describes the use of a single chain antibody (ScFv),
CC which is capable of recognizing a disease associated molecule in the
CC manufacture of a medicament for the prevention and treatment of a
CC disease condition. The ScFv antibody is useful in the manufacture of
CC a medicament, for affecting a disease in vivo, for preparing a
CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC treatment of a disease. The ScFv antibody is also useful for
CC treating inflammatory diseases including arthritis, hypersensitivity,
CC autoimmune diseases, cancers, central nervous system disorders
CC including Parkinson's disease, periodontal diseases, cardiopulmonary
CC diseases, cardiovascular diseases, gastrointestinal disorders,
CC infections, diabetes, Helicobacter-related diseases, and other immune
CC disorders. The present sequence represents a B7-2.5T4.1 fusion protein.
CC This comprises the N-terminus of the 5T4 ScFv is fused after amino acid
CC 215 of human B7-2.

XX SQ Sequence 246 AA;

Query Match 72.2%; Score 1252; DB 22; Length 246;
Best Local Similarity 100.0%; Pred. No. 9e-107;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGLSNILFVMAFLISGAAPLKIQAYFNETADLPQFANSQNSLSLVVFWQDQENLVN 66
DB 1 MGLSNILFVMAFLISGAAPLKIQAYFNETADLPQFANSQNSLSLVVFWQDQENLVN 60

QY 67 EYVLGKFKFDSVHSHKMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRIHO 126
DB 61 EYVLGKFKFDSVHSHKMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRIHO 120

QY 127 NSELSVLNFSQPEIPIVPSNITENVYINLTCSHIGYPKPKMSVLLRTKNSITIEDGIM 186
DB 121 NSELSVLNFSQPEIPIVPSNITENVYINLTCSHIGYPKPKMSVLLRTKNSITIEDGIM 180

QY 187 QKSDQNVTELYDVSISLSVSPDVTNNMTIFCILETDKTRLLSSPFSIELEDPQPPDHI 246
DB 181 QKSDQNVTELYDVSISLSVSPDVTNNMTIFCILETDKTRLLSSPFSIELEDPQPPDHI 240

QY 247 P 247
DB 241 P 241

RESULT 12
AAW90209
ID AAW90209 standard; Protein; 244 AA.
XX
AC AAW90209;
XX
XX 10-MAY-1999 (first entry)
XX
XX

```

DE  hb7.1his soluble fusion protein.
XX
XX  B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX  CD86; T cell activation; inhibitor; graft versus host disease;
XX  transplant rejection; allograft rejection; autoimmune disease;
XX  allergy; therapy; human; hb7.1his.
OS  Chimeric - Homo sapiens.
OS  Chimeric - synthetic.
XX
XX  Key Location/Qualifiers
XX  Peptide 1..23
XX  /note= "potential eukaryotic secretory signal
XX  Peptide"
XX  Domain 24..238
XX  /note= "human B7.2 (mature protein) extracellular
XX  Peptide 239..244
XX  /note= "histidine detection/purification tag"
XX
XX  WO9858965-A2.
XX
XX  30-DEC-1998.
XX
XX  22-JUN-1998; 98WO-EP03791.
XX
XX  20-JUN-1997; 97EP-0870092.
XX
XX  (INNO-) INNOGENETICS NV.
XX
XX  Bosman A, Buyse M, Lorre K, Sablon E;
XX  WPI; 1999-105615/09.
XX
XX  New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX  immune diseases including allograft rejection
XX
XX  Example 3.1.3; Fig 5; 182pp; English.
XX
XX  This 28 kDa soluble fusion protein, termed hb7.2his, is composed
XX  of human co-stimulatory molecule B7.2 extracellular domain fused
XX  C-terminally to a hexahistidine detection/purification tag. It
XX  was produced by PCR amplification (see AAX01603-04) of hb7.2 cDNA
XX  in pcDNAhB7.2 (ICCG3207), insertion of the PCR fragment into
XX  baculovirus transfer vector pACSG2 and expression in Sf9 Spodoptera
XX  frugiperda insect cells. The invention relates to molecules such
XX  as diabodies, trivalent and tetravalent antibodies and small
XX  antigen binding peptides which can cross-link, or cross-react
XX  with, B7.1 and B7.2 expressed on professional antigen presenting
XX  cells leading to the inhibition of antigen-specific T cell
XX  activation. Methods to produce such molecules are provided. The
XX  molecules are used to treat or prevent diseases of the immune
XX  system, in particular graft rejection, graft versus host disease,
XX  allergy and autoimmune diseases (claimed).
XX
XX  Sequence 244 AA;
XX
XX  Query Match 71.6%; Score 1241; DB 20; Length 244;
XX  Best Local Similarity 100.0%; Pred. No. 9.2e-106;
XX  Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 7 MGLSNILFWMAFLLSGAAPLKIQAFNETADLPQFANSQNSLSLVFWQDENLVLN 66
Db 1 MGLSNILFWMAFLLSGAAPLKIQAFNETADLPQFANSQNSLSLVFWQDENLVLN 60
Qy 67 EYVLGKEKEDSVHVKYMGRTSFDSDSWTLRLHLNLIQKGLYQCLIIHKKPTGMIHQH 126
Db 61 EYVLGKEKEDSVHVKYMGRTSFDSDSWTLRLHLNLIQKGLYQCLIIHKKPTGMIHQH 120
Qy 127 NSELSVLANFSQPEIVPISNITENVYINLTCSIIHGYPKPKMSVLLRTKNSITIEYDGM 186
Db 121 NSELSVLANFSQPEIVPISNITENVYINLTCSIIHGYPKPKMSVLLRTKNSITIEYDGM 180

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Qy 187 QXSQDNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPOPPDH 245
Db 181 QXSQDNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPOPPDH 239

RESULT 13
AAW90207
ID AAW90207 standard; Protein; 477 AA.
XX
XX  AC AAW90207;
XX
XX  DT 10-MAY-1999 (first entry)
XX
XX  DE hb7.2Fc soluble fusion protein.
XX
XX  KW B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX  CD86; T cell activation; inhibitor; graft versus host disease;
XX  transplant rejection; allograft rejection; autoimmune disease;
XX  allergy; therapy; human; antibody; hb7.1fc.
XX
XX  OS Chimeric - Homo sapiens.
XX  OS Chimeric - synthetic.
XX
XX  FH Key Location/Qualifiers
XX  FT Peptide 1..16
XX  /note= "potential eukaryotic secretory signal
XX  FT Peptide"
XX  FT Domain 17..239
XX  /note= "human B7.2 (mature protein) extracellular
XX  FT Peptide 240..245
XX  /note= "introduced by PCR cloning strategy"
XX  FT Protein 246..477
XX  /note= "human IgG1-Fc (hinge-CH2-CH3)"
XX
XX  PN WO9858965-A2.
XX
XX  PD 30-DEC-1998.
XX
XX  PF 22-JUN-1998; 98WO-EP03791.
XX
XX  PR 20-JUN-1997; 97EP-0870092.
XX
XX  PA (INNO-) INNOGENETICS NV.
XX
XX  PI Bosman A, Buyse M, Lorre K, Sablon E;
XX  WPI; 1999-105615/09.
XX
XX  DR New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX  immune diseases including allograft rejection
XX
XX  PS Example 3.1.1.3; Fig 3; 182pp; English.
XX
XX  CC This 54 kDa soluble fusion protein, termed hb7.2Fc, is composed of
XX  human co-stimulatory molecule B7.2 extracellular domain fused
XX  C-terminally to human IgG1-Fc. It was produced by PCR
XX  amplification of hb7.2 cDNA in plasmid pcDNAIneo-hB7.2, and
XX  insertion of the amplified cDNA into pVL-Fc (ICCG3048), resulting
XX  in pVLshB7.2-Fc (ICCG3004) baculovirus transfer plasmid. The invention
XX  relates to molecules such as diabodies, trivalent and tetravalent
XX  antibodies and small antigen binding peptides which can cross-link,
XX  or cross-react with, B7.1 and B7.2 expressed on professional
XX  antigen presenting cells leading to the inhibition of
XX  antigen-specific T cell activation. Methods to produce such
XX  molecules are provided. The molecules are used to treat or prevent
XX  diseases of the immune system, in particular graft rejection, graft
XX  versus host disease, allergy and autoimmune diseases (claimed).
XX
XX  SQ Sequence 477 AA;
XX
XX  Query Match 71.6%; Score 1241; DB 20; Length 477;
XX  Best Local Similarity 100.0%; Pred. No. 2.4e-105;

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Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 7 MGLSNILFVMAFLLSGAAPLKIOAYFNETADLP	COFANSQNSLSSELVWFVQDQENLVN 66
Db 1 MGLSNILFVMAFLLSGAAPLKIOAYFNETADLP	COFANSQNSLSSELVWFVQDQENLVN 60
QY 67 EYVLGKEKFDSDVHSGYMGRTSFDSDSWTLRLHNLOIKDGLYQCIIHHKXPTGMIRI	126
Db 61 EYVLGKEKFDSDVHSGYMGRTSFDSDSWTLRLHNLOIKDGLYQCIIHHKXPTGMIRI	120
QY 127 NSELSVLANFQPEIPTSINITENVYINLTCS	SIHGYPEPKMSVLLRTKNSIIEYDGM 186
Db 121 NSELSVLANFQPEIPTSINITENVYINLTCS	SIHGYPEPKMSVLLRTKNSIIEYDGM 180
QY 187 QKSQDNVTDELVDVSISSVSFPDVTNSMTIFCILETDKTRLLSPFSIELEDQPPPDH	245
Db 181 QKSQDNVTDELVDVSISSVSFPDVTNSMTIFCILETDKTRLLSPFSIELEDQPPPDH	239
RESULT 14	
AAW41076	
ID AAW41076 standard; protein; 329 AA.	
XX AC AAW41076;	
XX DT 20-DEC-1999 (first entry)	
XX DE Canine B7-2 protein.	
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease; allergic reaction; infectious disease; tumor development; canine; graft rejection; inflammation; arthritis; atopic dermatitis.	
OS Canis familiaris.	
XX WO9947558-A2.	
XX 23-SEP-1999.	
XX 19-MAR-1999; 99WO-US06187.	
PR 19-MAR-1998; 98US-0078765.	
PR 17-APR-1998; 98US-0062597.	
XX (HESK-) HESKA CORP.	
PI Sim G, Yang S, Sellins KS;	
PI WPI; 1999-571822/48.	
DR N-PSDB; AAZ27913, AAZ27915.	
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for treating, e.g. autoimmune and atopic diseases -	
PS Claim 4; Page 97-99; 148pp; English.	
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules and the encoded proteins can be used for preventing or treating diseases, e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor development, graft rejection, inflammation, arthritis and atopic diseases such as atopic dermatitis. They can be used in mammals such humans, dogs, cats, cattle, sheep or pets. The products can also be used for detection, diagnosis and drug screening.	
SQ Sequence 329 AA;	
Query/Match 57.9%; Score 1003; DB 20; Length 329;	
Best Local Similarity 62.3%; Pred. No. 1.1e-83;	
Matches 205; Conservative 47; Mismatches 71; Indels 6; Gaps 6;	
QY 4 QCTMGLSNILFVMAFLLSGAAPLKIOAYFNETADLP	COFANSQNSLSSELVWFVQDQENLVN 63

Db	4	RCITMELNNILFVMTLLLYGAAMKMSQAYFNKGTGELPCHFTNSQNSISDELVWFVQDQDKL	63
QY	64	VLNEVYLGRKEKFDSDVHSGYMGRTSFDSDWTLRLHNLOIKDGLYQCIIHHKXPTGMIRI	123
Db	64	VLTLYTRGKENPONVHRKYKRTSFDKDNWTLRLHNIQIKDGLYQCFVHHKPGKGLVPM	123
QY	124	QHMNSLSVLANFQPEIPTSINITENVYINLTCS	SIHGYPEPKMSVLLRTKNSIIEVDGIM 182
Db	124	QHMNSLSVLANFQPEIPTSINITENVYINLTCS	SIHGYPEPKMSVLLRTKNSIIEVDGIM 183
QY	183	DGTMQSDNVTELVDVSISSVSFPDVTNSMTIFCILETDKTRLLSPFSIELEDQPPPDH	241
Db	184	DTVMKSNQNVTELNVSISSVSFPDVTNSMTIFCILETDKTRLLSPFSIELEDQPPPDH	242
QY	242	PPDHIFWITAVL-PTVIICVMVFCLILMKWKKKRPRNSYKCGTNTMEREESEQTKKREK	300
Db	243	DGDHILWIAALLVLMVLICGMVFFLTURK-RKKQPGPSHECETNKVERKESEQTKERVR	301
QY	301	IHIPERSDEAQRVFKSKTSCDKSDTCF	329
Db	302	YHETERSDEAQCVC-NISKTAGDNNSTTQF	329
RESULT 15			
ID	AAW14944	standard; Protein; 250 AA.	
AC	AAW14944;		
DT	16-JUN-1997	(first entry)	
DE	Chimeric human/porcine CD86.		
XX	Xenotransplantation; graft rejection; cell interaction; pig; CD68; monoclonal antibody; chimeric antibody; diagnosis.		
OS	Chimeric Homo sapiens; Chimeric Sus scrofa.		
XX	Key	Location/Qualifiers	
FT	Peptide	1..25	
FT	Protein	/label= Sig_peptide	
FT	Region	26..250	
FT		/label= Mat_protein	
FT		246..250	
FT		/label= Histidine_tag	
PN	WO9711971-A1.		
PD	03-APR-1997.		
PF	27-SEP-1996;	96WO-US15575.	
PR	26-SEP-1996;	96US-0004489.	
PR	28-SEP-1995;	95US-0004489.	
XX	(ALEX-) ALEXION PHARM INC.		
PI	Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S; Rother RP;		
XX	WPI; 1997-212855/19.		
DR	N-PSDB; AAT62939.		
XX	Antibodies binding to porcine but not human cell interaction proteins - useful to treat and assay for rejection of xenografted porcine organs, tissues or cells		
PS	Disclosure; Page 69-70; 105pp; English.		
CC	A chimeric human/porcine CD86 (B7-2) cell adhesion molecule has amino acid residues 1-4 and 197-245 from human CD86, and amino		

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OM protein - protein search, using sw model

Run on: February 13, 2003, 11:32:49 ; Search time 18.0486 Seconds
(without alignments)
465.720 Million cell updates/sec

Title: US-09-425-516-2

Perfect score: 1733

Sequence: 1 MDPOCTWGLSNILFVMAFL.....AQRVFKSKTSCTSDKSDTCF 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubaa/US08_NEW PUB. pep.*
- 2: /cgn2_6/ptodata/2/pubaa/PCT NEW PUB. pep.*
- 3: /cgn2_6/ptodata/2/pubaa/US06_NEW PUB. pep.*
- 4: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB. pep.*
- 5: /cgn2_6/ptodata/2/pubaa/US07_NEW PUB. pep.*
- 6: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB. pep.*
- 7: /cgn2_6/ptodata/2/pubaa/PCTUS_PUBCOMB. pep.*
- 8: /cgn2_6/ptodata/2/pubaa/US08_PUBCOMB. pep.*
- 9: /cgn2_6/ptodata/2/pubaa/US09_NEW PUB. pep.*
- 10: /cgn2_6/ptodata/2/pubaa/US09_PUBCOMB. pep.*
- 11: /cgn2_6/ptodata/2/pubaa/US10_NEW PUB. pep.*
- 12: /cgn2_6/ptodata/2/pubaa/US10_PUBCOMB. pep.*
- 13: /cgn2_6/ptodata/2/pubaa/US60_NEW PUB. pep.*
- 14: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB. pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1733	100.0	329	8	US-08-592-711-4
2	1733	100.0	329	9	US-09-441-411-26
3	1733	100.0	329	10	US-09-837-867A-23
4	1696	97.9	323	9	US-09-896-738-11
5	1696	97.9	323	9	US-09-915-789A-16
6	1696	97.9	323	9	US-09-441-411-22
7	1696	97.9	323	10	US-09-955-866-5
8	1685.5	97.3	324	10	US-09-910-174A-6
9	1282	74.0	260	10	US-09-845-899A-5
10	1241	71.6	351	10	US-09-756-983-18
11	1148	66.2	219	9	US-09-915-789A-22
12	903	52.1	329	10	US-09-303-510-6
13	903	52.1	329	10	US-09-303-040-6
14	743.5	42.9	309	9	US-09-441-411-13
15	743.5	42.9	309	9	US-09-441-411-18
16	743.5	42.9	309	9	US-09-441-411-24
17	743.5	42.9	309	10	US-09-837-867A-21
18	724.5	41.8	314	9	US-09-441-411-14
19	724.5	41.8	314	9	US-09-441-411-19

20	724.5	41.8	314	10	US-09-837-867A-13	Sequence 13, Appl
21	715.5	41.3	356	9	US-09-441-411-11	Sequence 11, Appl
22	715.5	41.3	356	9	US-09-441-411-12	Sequence 12, Appl
23	715.5	41.3	356	9	US-09-441-411-16	Sequence 16, Appl
24	715.5	41.3	356	9	US-09-441-411-17	Sequence 17, Appl
25	710.5	41.0	303	9	US-09-441-411-15	Sequence 15, Appl
26	710.5	41.0	303	9	US-09-441-411-20	Sequence 20, Appl
27	328	18.9	61	10	US-09-837-867A-32	Sequence 32, Appl
28	245.5	14.2	320	10	US-09-837-867A-2	Sequence 2, Appl
29	244	14.1	306	10	US-09-837-867A-17	Sequence 17, Appl
30	224	12.9	292	10	US-09-303-510-2	Sequence 2, Appl
31	224	12.9	292	10	US-09-303-040-2	Sequence 2, Appl
32	222	12.8	292	10	US-09-303-510-4	Sequence 4, Appl
33	222	12.8	292	10	US-09-303-040-4	Sequence 4, Appl
34	201.5	11.6	288	8	US-08-592-711-2	Sequence 2, Appl
35	201.5	11.6	288	9	US-09-896-738-10	Sequence 10, Appl
36	201.5	11.6	288	9	US-09-915-789A-15	Sequence 15, Appl
37	201.5	11.6	288	10	US-09-772-102-14	Sequence 14, Appl
38	201.5	11.6	288	10	US-09-837-867A-19	Sequence 19, Appl
39	201.5	11.6	288	10	US-09-910-174A-5	Sequence 5, Appl
40	188	10.8	315	10	US-09-910-174A-28	Sequence 28, Appl
41	187	10.8	492	10	US-09-845-899A-3	Sequence 3, Appl
42	185.5	10.7	316	10	US-09-875-338-13	Sequence 13, Appl
43	183.5	10.6	226	9	US-09-915-789A-21	Sequence 21, Appl
44	183.5	10.6	316	10	US-09-875-338-11	Sequence 11, Appl
45	183.5	10.6	473	10	US-09-910-059-131	Sequence 131, App

ALIGNMENTS

RESULT 1

US-08-592-711-4

; Sequence 4, Application US/08592711

; Patent No. US20020115214A1

; GENERAL INFORMATION:

; APPLICANT: June, Carl H.

; APPLICANT: Thompson, Craig B.

; APPLICANT: Nabel, Gary J.

; APPLICANT: Gray, Gary S.

; APPLICANT: Rennert, Paul D.

; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/592,711

; FILING DATE: 26-JAN-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/435,816

; FILING DATE: 4-MAY-1995

; APPLICATION NUMBER: US 08/403,253

; FILING DATE: 10-MARCH-1995

; APPLICATION NUMBER: US 08/253,964

; FILING DATE: 3-JUNE-1994

; APPLICATION NUMBER: US 08/073,223

; FILING DATE: 4-JUNE-1993

; APPLICATION NUMBER: US 08/200,947

; FILING DATE: 23-FEB-1994

; APPLICATION NUMBER: US 07/864,805

; FILING DATE: 7-APR-1992

; APPLICATION NUMBER: US 08/247,505

; FILING DATE: 23-MAY-1994

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; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25-MAR-1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16-JUNE-1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23-NOV-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-592-711-4

Query Match 100.0%; Score 1733; DB 8; Length 329;
Best Local Similarity 100.0%; Pred. No. 1e-123;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 ENLVANEVYLGEKFDSDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
Db 61 ENLVANEVYLGEKFDSDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120

Qy 121 IRIHQMSSELSVLNFSQPEIVPISNITENVYINLTCSSIHGYPEPKMVSLLRTKNSTI 180
Db 121 IRIHQMSSELSVLNFSQPEIVPISNITENVYINLTCSSIHGYPEPKMVSLLRTKNSTI 180

Qy 181 EYDGIQKSDQNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPO 240
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Qy 241 PPPDHPITAVLPTVIIICVMVFCLILWKWKKKRPRNSYKCGTNTMEREESEQTKKREK 300
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Qy 301 IHIPERSDEAQRVFKSKTSKCDKSDTCF 329
Db 301 IHIPERSDEAQRVFKSKTSKCDKSDTCF 329

RESULT 2
US-09-441-411-26
; Sequence 26, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033,409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-441-411-26
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Best Local Similarity 100.0%; Pred. No. 1e-123;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 301 IHIPERSDEAQRVFKSKTSKCDKSDTCF 329
Db 301 IHIPERSDEAQRVFKSKTSKCDKSDTCF 329

RESULT 2
US-09-441-411-26
; Sequence 26, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033,409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-441-411-26
Query Match 100.0%; Score 1733; DB 9; Length 329;
Best Local Similarity 100.0%; Pred. No. 1e-123;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDPQCTMGLSNILFYMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSLVFWQDQ 60

Qy 61 ENLVANEVYLGEKFDSDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
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Qy 121 IRIHQMSSELSVLNFSQPEIVPISNITENVYINLTCSSIHGYPEPKMVSLLRTKNSTI 180
Db 121 IRIHQMSSELSVLNFSQPEIVPISNITENVYINLTCSSIHGYPEPKMVSLLRTKNSTI 180

Qy 181 EYDGIQKSDQNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPO 240
Db 181 EYDGIQKSDQNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPO 240

Qy 241 PPPDHPITAVLPTVIIICVMVFCLILWKWKKKRPRNSYKCGTNTMEREESEQTKKREK 300
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Qy 301 IHIPERSDEAQRVFKSKTSKCDKSDTCF 329
Db 301 IHIPERSDEAQRVFKSKTSKCDKSDTCF 329

RESULT 3
US-09-837-867A-23
; Sequence 23, Application US/09837867A
; Patent No. US20020098542A1
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Borriello, Francescopaulo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. US20020098542A1el Forms of T Cell Costimulatory
; TITLE OF INVENTION: Molecules and Uses Therefor
; FILE REFERENCE: BWI-120CPADV
; CURRENT APPLICATION NUMBER: US/09/837,867A
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 08/205,697
; PRIOR FILING DATE: 1994-03-02
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-837-867A-23

Query Match 100.0%; Score 1733; DB 10; Length 329;
Best Local Similarity 100.0%; Pred. No. 1e-123;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPQCTMGLSNILFYMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSLVFWQDQ 60
Db 1 MDPQCTMGLSNILFYMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSLVFWQDQ 60

Qy 61 ENLVANEVYLGEKFDSDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
Db 61 ENLVANEVYLGEKFDSDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120

Qy 121 IRIHQMSSELSVLNFSQPEIVPISNITENVYINLTCSSIHGYPEPKMVSLLRTKNSTI 180
Db 121 IRIHQMSSELSVLNFSQPEIVPISNITENVYINLTCSSIHGYPEPKMVSLLRTKNSTI 180

Qy 181 EYDGIQKSDQNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPO 240
Db 181 EYDGIQKSDQNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPO 240
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Db 181 EYDGMQSQDNVTLYDVSISLSVSPDVTNNMTFCILETDKTRLLSSPFSIELEDQP 240
Qy 241 PPDHLPWITAVLPTVIICVMVFCILLWKWKKKRPRNSYKCGTNTMEREESEOTKKREK 300
Db 241 PPDHLPWITAVLPTVIICVMVFCILLWKWKKKRPRNSYKCGTNTMEREESEOTKKREK 300
Qy 301 IHIPERSDEAQRVFKSSTSSCDKSDTCF 329
Db 301 IHIPERSDEAQRVFKSSTSSCDKSDTCF 329

RESULT 4
US-09-896-738-11
; Sequence 11, Application US/09896738
; Patent No. US20020165347A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Michael
; APPLICANT: Sullivan, John K.
; APPLICANT: Fang, Mei
; TITLE OF INVENTION: B7-Like Molecules and Uses Thereof
; FILE REFERENCE: 00-513-A
; CURRENT APPLICATION NUMBER: US/09/896,738
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,645
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-896-738-11

Query Match 97.9%; Score 1696; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 6.4e-121;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSLVFWQDQENLVN 66
Db 1 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSLVFWQDQENLVN 60
Qy 67 EYVLGKEKFDVSVHSGYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGMIRIHO 126
Db 61 EYVLGKEKFDVSVHSGYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGMIRIHO 120
Qy 127 NSELSVLANFSQPEIPIVPSINITENVYINLTCSISIHGYPEPKKMSVLLRTKNSITIEYDGM 186
Db 121 NSELSVLANFSQPEIPIVPSINITENVYINLTCSISIHGYPEPKKMSVLLRTKNSITIEYDGM 180
Qy 187 OKSQDNVTLYDVSISLSVSPDVTNNMTFCILETDKTRLLSSPFSIELEDPOPPDHI 246
Db 181 OKSQDNVTLYDVSISLSVSPDVTNNMTFCILETDKTRLLSSPFSIELEDPOPPDHI 240
Qy 247 PWITAVLPTVIICVMVFCILLWKWKKKRPRNSYKCGTNTMEREESEOTKKREKIHIPER 306
Db 241 PWITAVLPTVIICVMVFCILLWKWKKKRPRNSYKCGTNTMEREESEOTKKREKIHIPER 300

RESULT 5
US-09-441-411-22
; Sequence 22, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441.411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-441-411-22

Query Match 97.9%; Score 1696; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 6.4e-121;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSLVFWQDQENLVN 66
Db 1 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSLVFWQDQENLVN 60
Qy 67 EYVLGKEKFDVSVHSGYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGMIRIHO 126
Db 61 EYVLGKEKFDVSVHSGYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGMIRIHO 120
Qy 127 NSELSVLANFSQPEIPIVPSINITENVYINLTCSISIHGYPEPKKMSVLLRTKNSITIEYDGM 186
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; PRIOR APPLICATION NUMBER: US 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-789A-16

Query Match 97.9%; Score 1696; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 6.4e-121;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSLVFWQDQENLVN 66
Db 1 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSLVFWQDQENLVN 60
Qy 67 EYVLGKEKFDVSVHSGYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGMIRIHO 126
Db 61 EYVLGKEKFDVSVHSGYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGMIRIHO 120
Qy 127 NSELSVLANFSQPEIPIVPSINITENVYINLTCSISIHGYPEPKKMSVLLRTKNSITIEYDGM 186

RESULT 6
US-09-441-411-22
; Sequence 22, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441.411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-441-411-22

Query Match 97.9%; Score 1696; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 6.4e-121;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSLVFWQDQENLVN 66
Db 1 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSLVFWQDQENLVN 60
Qy 67 EYVLGKEKFDVSVHSGYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGMIRIHO 126
Db 61 EYVLGKEKFDVSVHSGYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGMIRIHO 120
Qy 127 NSELSVLANFSQPEIPIVPSINITENVYINLTCSISIHGYPEPKKMSVLLRTKNSITIEYDGM 186
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Db 121 NSELSVLNFSQPEIVPSNTENYVNLTCSSIHGYPEPKMSVLLRTKNSTIEYDGM 180
Qy 187 QKSQDNVTELYDVSISLSVSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDQPPPDHI 246
Db 181 QKSQDNVTELYDVSISLSVSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDQPPPDHI 240
Qy 247 PWITAVLPTVIICVMVFCILILWKWKKKRPRNSYKCGTNTMERESBOTKKREKIHIPER 306
Db 241 PWITAVLPTVIICVMVFCILILWKWKKKRPRNSYKCGTNTMERESBOTKKREKIHIPER 300
Qy 307 SDEAQRVFKSSKTSKCDKSDTCF 329
Db 301 SDEAQRVFKSSKTSKCDKSDTCF 323

RESULT 7
US-09-955-866-5
; Sequence 5, Application US/09955866
; Patent No. US20020107363A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Michael
; APPLICANT: Sullivan, John K.
; APPLICANT: Holst, Paige
; APPLICANT: Yoshinaga, Steven Kiyoshi
; TITLE OF INVENTION: B7-Like Polypeptides and Uses Thereof
; FILE REFERENCE: 00.759-A
; CURRENT APPLICATION NUMBER: US/09/955,866
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,867
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-866-5

Query Match 97.9%; Score 1696; DB 10; Length 323;
Best Local Similarity 100.0%; Pred. No. 6.4e-121;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSLVFWQDOENLVN 66
Db 1 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSLVFWQDOENLVN 60
Qy 67 EYVLGKEKFDVSVHSGYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRHQM 126
Db 61 EYVLGKEKFDVSVHSGYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRHQM 120
Qy 127 NSELSVLNFSQPEIVPSNTENYVNLTCSSIHGYPEPKMSVLLRTKNSTIEYDGM 186
Db 121 NSELSVLNFSQPEIVPSNTENYVNLTCSSIHGYPEPKMSVLLRTKNSTIEYDGM 180
Qy 187 QKSQDNVTELYDVSISLSVSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDQPPPDHI 246
Db 181 QKSQDNVTELYDVSISLSVSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDQPPPDHI 240
Qy 247 PWITAVLPTVIICVMVFCILILWKWKKKRPRNSYKCGTNTMERESBOTKKREKIHIPER 306
Db 241 PWITAVLPTVIICVMVFCILILWKWKKKRPRNSYKCGTNTMERESBOTKKREKIHIPER 300
Qy 307 SDEAQRVFKSSKTSKCDKSDTCF 329
Db 301 SDEAQRVFKSSKTSKCDKSDTCF 323

RESULT 8
US-09-910-174A-6
; Sequence 6, Application US/09910174A
; Patent No. US20020106730A1
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. US20020106730A1el Members of the B7
; FILE REFERENCE: 35800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174A
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-174A-6

Query Match 97.3%; Score 1685.5; DB 10; Length 324;
Best Local Similarity 99.7%; Pred. No. 4e-120;
Matches 323; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 7 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSLVFWQDOENLVN 66
Db 1 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSLVFWQDOENLVN 60
Qy 67 EYVLGKEKFDVSVHSGYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRHQM 126
Db 61 EYVLGKEKFDVSVHSGYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRHQM 120
Qy 127 NSELSVLNFSQPEIVPSNTENYVNLTCSSIHGYPEPKMSVLLRTKNSTIEYDGM 186
Db 121 NSELSVLNFSQPEIVPSNTENYVNLTCSSIHGYPEPKMSVLLRTKNSTIEYDGM 180
Qy 187 QKSQDNVTELYDVSISLSVSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDQPPPDHI 246
Db 181 QKSQDNVTELYDVSISLSVSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDQPPPDHI 240
Qy 247 PWITAVLPTVIICVMVFCILILWKWKKKRPRNSYKCGTNTMERESBOTKKREKIHIPER 305
Db 241 PWITAVLPTVIICVMVFCILILWKWKKKRPRNSYKCGTNTMERESBOTKKREKIHIPER 300
Qy 306 RSDEAQRVFKSSKTSKCDKSDTCF 329
Db 301 RSDEAQRVFKSSKTSKCDKSDTCF 324

RESULT 9
US-09-845-899A-5
; Sequence 5, Application US/09845899A
; Patent No. US20020147326A1
; GENERAL INFORMATION:
; APPLICANT: CHAIKIN, MARGERY ANN
; APPLICANT: LYN, SALLY DOREEN PATRICIA
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: HEXAMERIC FUSION PROTEINS AND USES
; FILE REFERENCE: P50496
; CURRENT APPLICATION NUMBER: US/09/845,899A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/202,346
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/043,948
; PRIOR FILING DATE: 1997-02-19
; PRIOR APPLICATION NUMBER: US 60/038,915
; PRIOR FILING DATE: 1997-02-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 260
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
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US-09-845-842A-5

Query Match 74.0%; Score 1282; DB 10; Length 260;
Best Local Similarity 99.6%; Pred. No. 8.8e-90;
Matches 246; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPQCTMGLSNILFWMAFLLSGAAPLKIQAIFYNETADLPCQFANSONQSLSELVVFWDQ 60
DB 1 MDPQCTMGLSNILFWMAFLLSGAAPLKIQAIFYNETADLPCQFANSONQSLSELVVFWDQ 60
QY 61 ENLVNEVYLKGEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKXPTGM 120
DB 61 ENLVNEVYLKGEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKXPTGM 120
QY 121 IRIHQNSELVLANFQSOPEIVPISNTENYINLTCSSIHGYPEPKKMSVLLRTKNSTI 180
DB 121 IRIHQNSELVLANFQSOPEIVPISNTENYINLTCSSIHGYPEPKKMSVLLRTKNSTI 180
QY 181 EYDGIQKSDQNVTELYDVSISSLVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPO 240
DB 181 EYDGIQKSDQNVTELYDVSISSLVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPO 240
QY 241 PPDHP 247
DB 241 PPDHP 247

RESULT 10
US-09-756-983-18
; Sequence 18, Application US/09756983
; Patent No. US20020122818A1
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR FILING DATE: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR FILING DATE: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: PCT/US99/2466
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion constructs with human and bacterial sequences
US-09-756-983-18

Query Match 71.6%; Score 1241; DB 10; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGLSNILFWMAFLLSGAAPLKIQAIFYNETADLPCQFANSONQSLSELVVFWDQENLVN 66
DB 1 MGLSNILFWMAFLLSGAAPLKIQAIFYNETADLPCQFANSONQSLSELVVFWDQENLVN 60
QY 67 EYVLGKEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKXPTGMIRHQM 126
DB 61 EYVLGKEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKXPTGMIRHQM 120
QY 127 NSELVLANFQSOPEIVPISNTENYINLTCSSIHGYPEPKKMSVLLRTKNSTIEYDGM 186
DB 121 NSELVLANFQSOPEIVPISNTENYINLTCSSIHGYPEPKKMSVLLRTKNSTIEYDGM 180
QY 187 QKSDQNVTELYDVSISSLVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPOPPDH 245

DB 181 QKSDQNVTELYDVSISSLVSPDVTSNMTIFCILETDKTRLLSSPFSIELEDPOPPDH 239

RESULT 11
US-09-915-789A-22
; Sequence 22, Application US/09915789A
; Patent No. US20020168762A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; FILE REFERENCE: 07039-219001
; CURRENT APPLICATION NUMBER: US/09/915,789A
; CURRENT FILING DATE: 2002-06-04
; PRIOR FILING DATE: 00/220,991
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-789A-22

Query Match 66.2%; Score 1148; DB 9; Length 219;
Best Local Similarity 100.0%; Pred. No. 9.4e-80;
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 QAYFNETADLPCQFANSONQSLSELVVFWDQENLVNEVYLKGEKFDVSHSKYMGRTSF 88
DB 1 QAYFNETADLPCQFANSONQSLSELVVFWDQENLVNEVYLKGEKFDVSHSKYMGRTSF 60
QY 89 DSDSWTLRLHNLQIKDKGLYQCIHHKXPTGMIRHQNSELVLANFQSOPEIVPISNIT 148
DB 61 DSDSWTLRLHNLQIKDKGLYQCIHHKXPTGMIRHQNSELVLANFQSOPEIVPISNIT 120
QY 149 ENVINLTCSSIHGYPEPKKMSVLLRTKNSTIEYDGMQKSDQNVTELYDVSISSLVSP 208
DB 121 ENVINLTCSSIHGYPEPKKMSVLLRTKNSTIEYDGMQKSDQNVTELYDVSISSLVSP 180
QY 209 DVTSNMTIFCILETDKTRLLSSPFSIELEDPOPPDH 247
DB 181 DVTSNMTIFCILETDKTRLLSSPFSIELEDPOPPDH 219

RESULT 12
US-09-303-510-6
; Sequence 6, Application US/09303510A
; Patent No. US20020028208A1
; GENERAL INFORMATION:
; APPLICANT: Collisson, Ellen W.
; APPLICANT: Choi, InSoo
; APPLICANT: Hash, Stephen M.
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline
; FILE REFERENCE: 54954
; CURRENT APPLICATION NUMBER: US/09/303,510A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,869
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Feline
US-09-303-510-6

Query Match 52.1%; Score 903; DB 10; Length 329;
Best Local Similarity 58.5%; Pred. No. 4.9e-61;
Matches 190; Conservative 44; Mismatches 83; Indels 8; Gaps 7;

QY 6 TMGLSNILFWMAFLLSGAAPLKIQAIFYNETADLPCQFANSONQSLSELVVFWDQENLVN 65

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Db      7  TWGLSHTLLVMAALLSGVSSMKSAQYFNKGTGELPCHFTNSQNSISLDELVWFWDQDKVL 66
Qy      66  NEVYLQKEKFDVSVHSGYMGRTSFDSDSWTLRLHNLQIKDGLYQCIIHHKKPTGMRIRHQ 125
Db      67  YEIFRCKENPQVHLKYKGRTSFDKDNWTLRLHNLVQIKDGYTHCFIHYGPKGLVPMHQ 126
Qy      126  MNSLSVLANFQSPQPIVPSINITENV-YINLTCSSIHGYPPEPKMSVLLRTKNSTIEYDG 184
Db      127  MSSDLVLANSFQPEITVTSNRTENSIGINLTCSSIOGYPEPKEMYQLANTENSTTKYDT 186
Qy      185  IMOKSDQNTVELYDVSISLSPDPVTSNMTIFCILETDKTR-LLSPFPFIELE--DPQP 241
Db      187  VMKKSQNNVTELYNYSILSPESVPE-AHNVSFVCALKLETLEMLLSLPFNIDAQPKDKDP 245
Qy      242  PPDIHWITAVLPT-VIICVMVFLIILWKWKKKRPNRSYKCGTNTWERESESQTKKREK 300
Db      246  EQGHFLWIAAVLVMFVFCGMVSFKTLRK-RKKQPGPSHECETIKRERKESQTNERYP 304
Qy      301  IHIPERSDEAQRVFKSSVTSSCDKS 325
Db      305  YHVPERSEDAQCV-NILKTASGDKN 328

RESULT 13
US-09-303-040-6
; Sequence 6, Application US/09303040
; Patent No. US20020051792A1
; GENERAL INFORMATION:
; APPLICANT: Winslow, Barbara J.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, Feline CTLA-4 or
; FILE REFERENCE: 54957-B
; CURRENT APPLICATION NUMBER: US/09/303,040
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,870
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 329
; TYPE: PRT
; ORGANISM: feline CD86
US-09-303-040-6

Query Match      52.1%; Score 903; DB 10; Length 329;
Best Local Similarity 58.5%; Pred. No. 4.9e-61;
Matches 190; Conservative 44; Mismatches 83; Indels 8; Gaps 7;

Qy      6  TWGLSNILFMAFLISGAAPLKIQAIFYNETADLPQOFANSONQSLSLSELVVFWQDQNLVL 65
Db      7  TWGLSHTLLVMAALLSGVSSMKSAQYFNKGTGELPCHFTNSQNSISLDELVWFWDQDKVL 66
Qy      66  NEVYLQKEKFDVSVHSGYMGRTSFDSDSWTLRLHNLQIKDGLYQCIIHHKKPTGMRIRHQ 125
Db      67  YEIFRCKENPQVHLKYKGRTSFDKDNWTLRLHNLVQIKDGYTHCFIHYGPKGLVPMHQ 126
Qy      126  MNSLSVLANFQSPQPIVPSINITENV-YINLTCSSIHGYPPEPKMSVLLRTKNSTIEYDG 184
Db      127  MSSDLVLANSFQPEITVTSNRTENSIGINLTCSSIOGYPEPKEMYQLANTENSTTKYDT 186
Qy      185  IMOKSDQNTVELYDVSISLSPDPVTSNMTIFCILETDKTR-LLSPFPFIELE--DPQP 241
Db      187  VMKKSQNNVTELYNYSILSPESVPE-AHNVSFVCALKLETLEMLLSLPFNIDAQPKDKDP 245
Qy      242  PPDIHWITAVLPT-VIICVMVFLIILWKWKKKRPNRSYKCGTNTWERESESQTKKREK 300
Db      246  EQGHFLWIAAVLVMFVFCGMVSFKTLRK-RKKQPGPSHECETIKRERKESQTNERYP 304
Qy      301  IHIPERSDEAQRVFKSSVTSSCDKS 325

Query Match      52.1%; Score 903; DB 10; Length 329;
Best Local Similarity 58.5%; Pred. No. 4.9e-61;
Matches 190; Conservative 44; Mismatches 83; Indels 8; Gaps 7;

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Db      305  YHVPERSEDAQCV-NILKTASGDKN 328

RESULT 14
US-09-441-411-13
; Sequence 13, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-13

Query Match      42.9%; Score 743.5; DB 9; Length 309;
Best Local Similarity 51.5%; Pred. No. 5e-49;
Matches 159; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

Qy      1  MDQCTWGLSNILFMAFLISGAAPLKIQAIFYNETADLPQOFANSONQSLSLSELVVFWQDQ 60
Db      1  MDPRCTMGALILFVTVLLISDAVSVEQAYFNGTAYLPCPFTKAQNTLSLSELVVFWQDQ 60
Qy      61  ENLVLNEVYLQKEKFDVSVHSGYMGRTSFDSDSWTLRLHNLQIKDGLYQCIIHHKKPTGM 120
Db      61  QKLVLYEHLGTEKLDVSNAKVLGRTSFDNNNTLRLHNVQIKDNGSYDCFIQKKPPTS 120
Qy      121  IRIHOMNSLSVLANFQSPQPIVPSINITENVYINLTCSSIHGYPPEPKMSVLLRTKNSTI 180
Db      121  IILQOTLTLSLVIANFSEPEIKLAQNTGNSGINLTCTSKQGHKPKKMYFLI--TNSTN 178
Qy      181  EYDGIWQKSQDNVTELYDVSISLSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDPPQ 240
Db      179  EYGDNQIISQDNVTELYDVSISLSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDPPQ 238
Qy      241  PPPDHPW--ITAVLPTVLIICVMVFLIILWKWKKKRPNRSYKCGTNTWERESESQTKKR 298
Db      239  P---QTYWKEITASVTVALLVML--LIIVCHKKPNQPSRP-----SNTASKLERDSNADR 289
Qy      299  EKIHIPE 305
Db      290  ETINLKE 296

RESULT 15
US-09-441-411-18
; Sequence 18, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-18

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Query Match 42.9%; Score 743.5; DB 9; Length 309;
Best Local Similarity 51.5%; Pred. No. 5e-49;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

Qy	1	MDPQCTMGLSNLTFVMAFLLSGAAPLKIQAYFNETADLPQCFANSQNSLSSELVVFWDQDQ	60
Db	1	MDPRCTMGLAILIFVTVILLISDAVSVEVETQAYFNGTAYLPCPFTKAQNISLSSELVVFWDQDQ	60
Qy	61	ENLVNLNEVYLKGKFDSDSVHSGMGRSTFSDSDSWTLRLHNLQIKDKGLYOCIIHHKKPTGM	120
Db	61	QKLVLYEHLGTEKLDSDVNAKYLGRSTFSDRNWTLRLHNVQIKDNGSYDCFIQKKPTGS	120
Qy	121	IRIQMNSLSVLNFSQPEIVPISNITENVYINLTCSSIHGYPEPKQMSVLLRTKNSTI	180
Db	121	IILQOQLTELSVIANFSEPEIKLAQNVYTGNSGINLTCTSKQGHKPKQMYFLI--TNSTN	178
Qy	181	EYDGINMQSDNVTELYDVVISLSVSPDPVTSNMTIFCILETDKTRLSSPFSIELEDPO	240
Db	179	EYGDNQIISQDNVTLEFISISLSLSLSPDGVWMTVCVLETESMKISSKPLNFTOEFFS	238
Qy	241	PPDPHIPW--ITAVLPTVIIQWVFCILMLWKKKKRPNSYKCGTNTMERESEOTKKR	298
Db	239	P---QTYWKEITASVTVALLVWL--LIIVCHKKKNQPSRP----SNTASKLERDSNADR	289
Qy	299	EKIHIPE	305
Db	290	ETINLKE	296

Search completed: February 13, 2003, 11:39:57
Job time : 19.0486 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 11:29:49 ; Search time 12.8918 Seconds
(without alignments)
750.873 Million cell updates/sec

Title: US-09-425-516-2

Perfect score: 1733
Sequence: 1 MDPQTMGLSNILFVMAFL.....AQRVFKSKTSCDKSDTCF 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata1/1/aa/5A_COMB.pep.*
2: /cgn2_6/ptodata1/1/aa/5B_COMB.pep.*
3: /cgn2_6/ptodata1/1/aa/6A_COMB.pep.*
4: /cgn2_6/ptodata1/1/aa/6B_COMB.pep.*
5: /cgn2_6/ptodata1/1/aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata1/1/aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1733	100.0	329	2 US-08-456-104-2	Sequence 2, Appli
2	1733	100.0	329	2 US-08-101-624-2	Sequence 2, Appli
3	1733	100.0	329	3 US-08-479-744A-2	Sequence 2, Appli
4	1733	100.0	329	4 US-08-280-757B-2	Sequence 2, Appli
5	1733	100.0	329	4 US-08-205-697A-23	Sequence 23, Appl
6	1733	100.0	329	4 US-08-702-525-23	Sequence 23, Appl
7	1733	100.0	329	4 US-08-403-253A-4	Sequence 4, Appli
8	1733	100.0	329	5 PCT-US95-02576-23	Sequence 23, Appl
9	1696	97.9	323	4 US-09-651-200-21	Sequence 21, Appl
10	1696	97.9	323	5 PCT-US94-09642-2	Sequence 2, Appli
11	1003	57.9	329	4 US-09-651-200-19	Sequence 19, Appl
12	953	55.0	325	4 US-09-651-200-20	Sequence 20, Appl
13	903	52.1	329	4 US-09-651-200-18	Sequence 4, Appli
14	743.5	42.9	309	2 US-08-456-104-4	Sequence 4, Appli
15	743.5	42.9	309	3 US-08-479-744A-23	Sequence 23, Appl
16	743.5	42.9	309	4 US-08-280-757B-23	Sequence 23, Appl
17	743.5	42.9	309	4 US-08-205-697A-21	Sequence 21, Appl
18	743.5	42.9	309	4 US-08-702-525-21	Sequence 21, Appl
19	743.5	42.9	309	5 PCT-US95-02576-21	Sequence 21, Appl
20	743.5	42.9	309	5 PCT-US95-02576-13	Sequence 13, Appl
21	724.5	41.8	314	4 US-08-205-697A-13	Sequence 13, Appl
22	724.5	41.8	314	4 US-08-702-525-13	Sequence 13, Appl
23	724.5	41.8	314	5 PCT-US95-02576-13	Sequence 13, Appl
24	710.5	41.0	303	4 US-09-651-200-23	Sequence 23, Appl
25	577	33.3	110	3 US-08-479-744A-45	Sequence 45, Appl
26	577	33.3	110	4 US-08-280-757B-45	Sequence 45, Appl
27	517	29.8	102	3 US-08-479-744A-47	Sequence 47, Appl

28	517	29.8	102	4	US-08-280-757B-47	Sequence 47, Appl
29	328	18.9	61	4	US-08-205-697A-32	Sequence 32, Appl
30	328	18.9	61	4	US-08-702-525-32	Sequence 32, Appl
31	328	18.9	61	5	PCT-US95-02576-32	Sequence 32, Appl
32	324	18.7	95	4	US-08-928-383B-10	Sequence 10, Appl
33	245.5	14.2	320	4	US-08-205-697A-2	Sequence 2, Appli
34	245.5	14.2	320	4	US-08-702-525-2	Sequence 2, Appli
35	245.5	14.2	320	5	PCT-US95-02576-2	Sequence 2, Appli
36	244	14.1	306	4	US-08-205-697A-17	Sequence 17, Appl
37	244	14.1	306	4	US-08-702-525-17	Sequence 17, Appl
38	244	14.1	306	4	US-09-651-200-17	Sequence 17, Appl
39	244	14.1	306	5	PCT-US95-02576-17	Sequence 17, Appl
40	243	14.0	299	4	US-09-651-200-15	Sequence 15, Appl
41	242	14.0	306	2	US-08-147-772-4	Sequence 4, Appli
42	242	14.0	306	2	US-08-456-104-8	Sequence 8, Appli
43	242	14.0	306	2	US-08-101-624-25	Sequence 25, Appl
44	242	14.0	306	3	US-08-153-262-4	Sequence 4, Appli
45	242	14.0	306	3	US-08-479-744A-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1

US-08-456-104-2
; Sequence 2, Application US/08456104
; Patent No. 5861310
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/456,104
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624;
; FILING DATE: 26-JUL-1993;
; APPLICATION NUMBER: 08/109,393;
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-456-104-2

Query Match 100.0%; Score 1733; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.3e-154;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPCQTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQFANSONQSLSELVFWQDQ 60
Db 1 MDPCQTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQFANSONQSLSELVFWQDQ 60
QY 61 ENLVLNEVYLGRKEFDSVHSKYMGRTSFSDSWTLRLHNLQIKDKGLYQCCIHHKKPTGM 120
Db 61 ENLVLNEVYLGRKEFDSVHSKYMGRTSFSDSWTLRLHNLQIKDKGLYQCCIHHKKPTGM 120
QY 121 IRIHQNSELVLNANFSOPEIPIVPSINITENNYINLTCSSIHGYPEPKKMSVLLRTKNSTI 180
Db 121 IRIHQNSELVLNANFSOPEIPIVPSINITENNYINLTCSSIHGYPEPKKMSVLLRTKNSTI 180
QY 181 EYDGMQSDQNVTELYDVSISSVSFPDVTNNMTIFCILETDKTRLLSSPFSIELEDPO 240
Db 181 EYDGMQSDQNVTELYDVSISSVSFPDVTNNMTIFCILETDKTRLLSSPFSIELEDPO 240
QY 241 PPPDHIPWITAVLPTVIIICVMVFCLILWKWKKKRPRNSYKCGTNTWEREESQTKKREK 300
Db 241 PPPDHIPWITAVLPTVIIICVMVFCLILWKWKKKRPRNSYKCGTNTWEREESQTKKREK 300
QY 301 IHIPERSDEAQRVFKSKTSCKDSQTCF 329
Db 301 IHIPERSDEAQRVFKSKTSCKDSQTCF 329

RESULT 2

US-08-101-624-2
; Sequence 2, Application US/08101624
; Patent No. 5942607
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 5942607el CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/101,624
; FILING DATE: 26-JUL-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-101-624-2

Query Match 100.0%; Score 1733; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.3e-154;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPCQTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQFANSONQSLSELVFWQDQ 60
Db 1 MDPCQTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQFANSONQSLSELVFWQDQ 60
QY 61 ENLVLNEVYLGRKEFDSVHSKYMGRTSFSDSWTLRLHNLQIKDKGLYQCCIHHKKPTGM 120
Db 61 ENLVLNEVYLGRKEFDSVHSKYMGRTSFSDSWTLRLHNLQIKDKGLYQCCIHHKKPTGM 120
QY 121 IRIHQNSELVLNANFSOPEIPIVPSINITENNYINLTCSSIHGYPEPKKMSVLLRTKNSTI 180
Db 121 IRIHQNSELVLNANFSOPEIPIVPSINITENNYINLTCSSIHGYPEPKKMSVLLRTKNSTI 180
QY 181 EYDGMQSDQNVTELYDVSISSVSFPDVTNNMTIFCILETDKTRLLSSPFSIELEDPO 240
Db 181 EYDGMQSDQNVTELYDVSISSVSFPDVTNNMTIFCILETDKTRLLSSPFSIELEDPO 240
QY 241 PPPDHIPWITAVLPTVIIICVMVFCLILWKWKKKRPRNSYKCGTNTWEREESQTKKREK 300
Db 241 PPPDHIPWITAVLPTVIIICVMVFCLILWKWKKKRPRNSYKCGTNTWEREESQTKKREK 300
QY 301 IHIPERSDEAQRVFKSKTSCKDSQTCF 329
Db 301 IHIPERSDEAQRVFKSKTSCKDSQTCF 329

RESULT 3

US-08-479-744A-2
; Sequence 2, Application US/08479744A
; Patent No. 6084067
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,744A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/280,757
; FILING DATE: 26-JUL-1994
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 28-AUG-1993
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-479-744A-2

Query Match 100.0%; Score 1733; DB 3; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.3e-154;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPOCTMGLSNILFVMAFLSLGAAPLKIQAYFNETADLPCQFANSQNSQSLSELVVFWDQ 60
DB 1 MDPOCTMGLSNILFVMAFLSLGAAPLKIQAYFNETADLPCQFANSQNSQSLSELVVFWDQ 60
QY 61 ENLVNEVYLKGEKFDSDVSHSKYMGRTSFDSWTLRLHNLQIKDGLYQCIHHKKPTGM 120
DB 61 ENLVNEVYLKGEKFDSDVSHSKYMGRTSFDSWTLRLHNLQIKDGLYQCIHHKKPTGM 120
QY 121 IRIHQMSSELSVLANFSPQEIPIVPSINITENVYINLTCSHIGYPEPKMSVLLRTKNSTI 180
DB 121 IRIHQMSSELSVLANFSPQEIPIVPSINITENVYINLTCSHIGYPEPKMSVLLRTKNSTI 180
QY 181 EYDGMQSDQNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSPFSIELEDPO 240
DB 181 EYDGMQSDQNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSPFSIELEDPO 240
QY 241 PPPDHIPWITAVLPTVILCVMVFCILILWKWKKKRPRNSYKCGTNTMEREESEQTKKREK 300
DB 241 PPPDHIPWITAVLPTVILCVMVFCILILWKWKKKRPRNSYKCGTNTMEREESEQTKKREK 300
QY 301 IHIPERSDEAQRVFKSSKTSCKSDTCF 329
DB 301 IHIPERSDEAQRVFKSSKTSCKSDTCF 329

RESULT 4

US-08-280-757B-2

; Sequence 2, Application US/08280757B
; Patent No. 6130316
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; APPLICANT: Greenfield, Edward
; TITLE OF INVENTION: No. 6130316el CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/280,757B
; FILING DATE: 26-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP2
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-280-757B-2

Query Match 100.0%; Score 1733; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.3e-154;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPOCTMGLSNILFVMAFLSLGAAPLKIQAYFNETADLPCQFANSQNSQSLSELVVFWDQ 60
DB 1 MDPOCTMGLSNILFVMAFLSLGAAPLKIQAYFNETADLPCQFANSQNSQSLSELVVFWDQ 60
QY 61 ENLVNEVYLKGEKFDSDVSHSKYMGRTSFDSWTLRLHNLQIKDGLYQCIHHKKPTGM 120
DB 61 ENLVNEVYLKGEKFDSDVSHSKYMGRTSFDSWTLRLHNLQIKDGLYQCIHHKKPTGM 120
QY 121 IRIHQMSSELSVLANFSPQEIPIVPSINITENVYINLTCSHIGYPEPKMSVLLRTKNSTI 180
DB 121 IRIHQMSSELSVLANFSPQEIPIVPSINITENVYINLTCSHIGYPEPKMSVLLRTKNSTI 180
QY 181 EYDGMQSDQNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSPFSIELEDPO 240
DB 181 EYDGMQSDQNVTELYDVSISLSVSPDVTSNMTIFCILETDKTRLLSPFSIELEDPO 240
QY 241 PPPDHIPWITAVLPTVILCVMVFCILILWKWKKKRPRNSYKCGTNTMEREESEQTKKREK 300
DB 241 PPPDHIPWITAVLPTVILCVMVFCILILWKWKKKRPRNSYKCGTNTMEREESEQTKKREK 300
QY 301 IHIPERSDEAQRVFKSSKTSCKSDTCF 329
DB 301 IHIPERSDEAQRVFKSSKTSCKSDTCF 329

RESULT 5

US-08-205-697A-23

; Sequence 23, Application US/08205697A
; Patent No. 6218510
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Borriello, Francescopaulo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
; TITLE OF INVENTION: and Uses Therefor
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/205,697A
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-205-697A-23

Query Match 100.0%; Score 1733; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.3e-154; Indels 0; Gaps 0;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPOCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSONQSLSSELVFWQDQ 60
Db 1 MDPOCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSONQSLSSELVFWQDQ 60

QY 61 ENLVNNEVYLGKEKEDSVHSGYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGM 120
Db 61 ENLVNNEVYLGKEKEDSVHSGYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGM 120

QY 121 IRIHOMNSELVLANFQSEIPIVPSNITENVYINLTCSIIHGYPEPKMSVLLRTKNSTI 180
Db 121 IRIHOMNSELVLANFQSEIPIVPSNITENVYINLTCSIIHGYPEPKMSVLLRTKNSTI 180

QY 181 EYDGIHQKSDQNVTELYDVSIISVSFDPVTSNMTIFCILETDKTRLLSSPFSIELEDPO 240
Db 181 EYDGIHQKSDQNVTELYDVSIISVSFDPVTSNMTIFCILETDKTRLLSSPFSIELEDPO 240

QY 241 PPPDHIPWITAVLPTVTCVWVFCILILWKMKKKRPRNSYKCGTNTWEREESQTKKREK 300
Db 241 PPPDHIPWITAVLPTVTCVWVFCILILWKMKKKRPRNSYKCGTNTWEREESQTKKREK 300

QY 301 IHIPERSDEAQRVFKSKTSCKDSDTCF 329
Db 301 IHIPERSDEAQRVFKSKTSCKDSDTCF 329

RESULT 6

US-08-702-525-23
; Sequence 23, Application US/08702525
; Patent No. 6294660
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Sharpe
; APPLICANT: Borriello, Francescopaolo
; APPLICANT: Freeman, Gordon
; APPLICANT: Nadler, Lee
; TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory
; TITLE OF INVENTION: Molecules and Uses Therefor
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,525
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy B.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWT-120CPUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-525-23

Query Match 100.0%; Score 1733; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.3e-154; Indels 0; Gaps 0;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPOCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSONQSLSSELVFWQDQ 60
Db 1 MDPOCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSONQSLSSELVFWQDQ 60

QY 61 ENLVNNEVYLGKEKEDSVHSGYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGM 120
Db 61 ENLVNNEVYLGKEKEDSVHSGYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGM 120

QY 121 IRIHOMNSELVLANFQSEIPIVPSNITENVYINLTCSIIHGYPEPKMSVLLRTKNSTI 180
Db 121 IRIHOMNSELVLANFQSEIPIVPSNITENVYINLTCSIIHGYPEPKMSVLLRTKNSTI 180

QY 181 EYDGIHQKSDQNVTELYDVSIISVSFDPVTSNMTIFCILETDKTRLLSSPFSIELEDPO 240
Db 181 EYDGIHQKSDQNVTELYDVSIISVSFDPVTSNMTIFCILETDKTRLLSSPFSIELEDPO 240

QY 241 PPPDHIPWITAVLPTVTCVWVFCILILWKMKKKRPRNSYKCGTNTWEREESQTKKREK 300
Db 241 PPPDHIPWITAVLPTVTCVWVFCILILWKMKKKRPRNSYKCGTNTWEREESQTKKREK 300

QY 301 IHIPERSDEAQRVFKSKTSCKDSDTCF 329
Db 301 IHIPERSDEAQRVFKSKTSCKDSDTCF 329

RESULT 7

US-08-403-253A-4
; Sequence 4, Application US/08403253A
; Patent No. 6352694
; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; APPLICANT: Gray, Gary S., Remmert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,253A
; FILING DATE: March 10, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505

; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-403-253A-4

Query Match 100.0%; Score 1733; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.3e-154;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPOCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSONQSLSELVVFWDQ 60
DB 1 MDPOCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSONQSLSELVVFWDQ 60

QY 61 ENLVLENYVLGKEKEDSVHSHYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
DB 61 ENLVLENYVLGKEKEDSVHSHYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120

QY 121 IRIHQNSELVLANFPOPEIVPISNITENVYINLTCSHIGYPPEPKMSVLLRTKNTI 180
DB 121 IRIHQNSELVLANFPOPEIVPISNITENVYINLTCSHIGYPPEPKMSVLLRTKNTI 180

QY 181 EYDGMQSDQNVTELYDVSISLSVSPDVTSMNIFCILETDKTRLLSPFSIELEDPO 240
DB 181 EYDGMQSDQNVTELYDVSISLSVSPDVTSMNIFCILETDKTRLLSPFSIELEDPO 240

QY 241 PPPDHIPWITAVLPVTCVWVFCILWKKKKRPRNSYKCGTNTMERESSEQTKKREK 300
DB 241 PPPDHIPWITAVLPVTCVWVFCILWKKKKRPRNSYKCGTNTMERESSEQTKKREK 300

QY 301 IHIPERSDEAQRVFKSSKTSCKSDTCF 329
DB 301 IHIPERSDEAQRVFKSSKTSCKSDTCF 329

RESULT 8
PCT-US95-02576-23
; Sequence 23, Application PC/TUS9502576
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
; TITLE OF INVENTION: and Uses therefor
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02576
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120CPPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-02576-23

Query Match 100.0%; Score 1733; DB 5; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.3e-154;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPOCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSONQSLSELVVFWDQ 60
DB 1 MDPOCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSONQSLSELVVFWDQ 60

QY 61 ENLVLENYVLGKEKEDSVHSHYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
DB 61 ENLVLENYVLGKEKEDSVHSHYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120

QY 121 IRIHQNSELVLANFPOPEIVPISNITENVYINLTCSHIGYPPEPKMSVLLRTKNTI 180
DB 121 IRIHQNSELVLANFPOPEIVPISNITENVYINLTCSHIGYPPEPKMSVLLRTKNTI 180

QY 181 EYDGMQSDQNVTELYDVSISLSVSPDVTSMNIFCILETDKTRLLSPFSIELEDPO 240
DB 181 EYDGMQSDQNVTELYDVSISLSVSPDVTSMNIFCILETDKTRLLSPFSIELEDPO 240

QY 241 PPPDHIPWITAVLPVTCVWVFCILWKKKKRPRNSYKCGTNTMERESSEQTKKREK 300
DB 241 PPPDHIPWITAVLPVTCVWVFCILWKKKKRPRNSYKCGTNTMERESSEQTKKREK 300

QY 301 IHIPERSDEAQRVFKSSKTSCKSDTCF 329
DB 301 IHIPERSDEAQRVFKSSKTSCKSDTCF 329

RESULT 9
US-09-651-200-21
; Sequence 21, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651,200
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 21

; LENGTH: 323
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-651-200-21

Query Match 97.9%; Score 1696; DB 4; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.2e-150;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MGLSNILFWMAFLLSGAAPLKIQAYFNETADLPFCOFANSONOSLSLSELVFWQDOENLVN 66
Db 1 MGLSNILFWMAFLLSGAAPLKIQAYFNETADLPFCOFANSONOSLSLSELVFWQDOENLVN 60

Qy 67 EYVLGKEKFDSDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRHQM 126
Db 61 EYVLGKEKFDSDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRHQM 120

Qy 127 NSELSVLNFSOPEIPIISNTENYVNLTCSSIHGYPEPKKMSVLLRTKNSTIEYDGIM 186
Db 121 NSELSVLNFSOPEIPIISNTENYVNLTCSSIHGYPEPKKMSVLLRTKNSTIEYDGIM 180

Qy 187 QKSQDNVTLEYDVSISLSVSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDPOPPPDHI 246
Db 181 QKSQDNVTLEYDVSISLSVSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDPOPPPDHI 240

Qy 247 PWITAVLPTVILCVMVFCILILWKWKXKPRNSYKCGTNTWERESEQTKKREKIHIPER 306
Db 241 PWITAVLPTVILCVMVFCILILWKWKXKPRNSYKCGTNTWERESEQTKKREKIHIPER 300

Qy 307 SDEAQRVFKSKTSCKSDTCF 329
Db 301 SDEAQRVFKSKTSCKSDTCF 323

RESULT 10

PCT-US94-09642-2
; Sequence 2, Application PC/TUS9409642
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Purified Mammalian CTLA-4 Binding
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation, M-3-W
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940-1000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh Iici
; OPERATING SYSTEM: System Software 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09642
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/120,606
; FILING DATE: 13-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/116,882
; FILING DATE: 03-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Blasdale, John H. C.
; REGISTRATION NUMBER: 31,895
; REFERENCE/DOCKET NUMBER: DX0390K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-822-7398
; TELEFAX: 201-822-7039
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 323 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-09642-2

Query Match 97.9%; Score 1696; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.2e-150;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MGLSNILFWMAFLLSGAAPLKIQAYFNETADLPFCOFANSONOSLSLSELVFWQDOENLVN 66
Db 1 MGLSNILFWMAFLLSGAAPLKIQAYFNETADLPFCOFANSONOSLSLSELVFWQDOENLVN 60

Qy 67 EYVLGKEKFDSDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRHQM 126
Db 61 EYVLGKEKFDSDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRHQM 120

Qy 127 NSELSVLNFSOPEIPIISNTENYVNLTCSSIHGYPEPKKMSVLLRTKNSTIEYDGIM 186
Db 121 NSELSVLNFSOPEIPIISNTENYVNLTCSSIHGYPEPKKMSVLLRTKNSTIEYDGIM 180

Qy 187 QKSQDNVTLEYDVSISLSVSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDPOPPPDHI 246
Db 181 QKSQDNVTLEYDVSISLSVSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDPOPPPDHI 240

Qy 247 PWITAVLPTVILCVMVFCILILWKWKXKPRNSYKCGTNTWERESEQTKKREKIHIPER 306
Db 241 PWITAVLPTVILCVMVFCILILWKWKXKPRNSYKCGTNTWERESEQTKKREKIHIPER 300

Qy 307 SDEAQRVFKSKTSCKSDTCF 329
Db 301 SDEAQRVFKSKTSCKSDTCF 323

RESULT 11

US-09-651-200-19
; Sequence 19, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651,200
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-651-200-19

Query Match 57.9%; Score 1003; DB 4; Length 329;
Best Local Similarity 62.3%; Pred. No. 7.9e-86;
Matches 205; Conservative 47; Mismatches 71; Indels 6; Gaps 6;

Qy 4 QCTMGLSNILFWMAFLLSGAAPLKIQAYFNETADLPFCOFANSONOSLSLSELVFWQDOENL 63
Db 4 RCTMGLSNILFWMAFLLSGAAPLKIQAYFNETADLPFCOFANSONOSLSLSELVFWQDOENL 63

Qy 64 VLAENVLGKKEKFDSDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIR 123
Db 64 VLYELRYGKNGENPQNVHRKYKGRTSFDKDNWTLRLHNIQIKDKGLYQCFVHHKPGKGLVPM 123

Qy 124 HONNELSVANFSPQEIPIVPSNITENV-YINLTCSSIHGYPEPKKMSVLLRTKNSITIEY 182
Db 124 HONNELSVANFSPQEIPIVPSNITENV-YINLTCSSIHGYPEPKKMSVLLRTKNSITIEY 183
Qy 183 DGMKQSDNVTLYDVSISLVSFPDVTNSMTIFCILETKRLSSPFSIELE-DPOP 241
Db 184 DTMKQSDNVTLYDVSISLVSFPDVTNSMTIFCILETKRLSSPFSIELE-DPOP 242
Qy 242 PDHPIWITAVLPT-VIIICVMVFCILILMKKKKPRNSYKCGTNTMERESQTKKREK 300
Db 243 DGHILWIAALLVWLILCGWVFLTLRK-RKKQPGPSHECETIKRKERKESQTKNERVP 301
Qy 301 IHIPERSDEAQRVFKSKTSSTSSCDKSCF 329
Db 302 YHETERSDEAQC-VNISKTAGSDNSTTQF 329

RESULT 12

US-09-651-200-20
; Sequence 20, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-562 (CIPA-62)
; CURRENT APPLICATION NUMBER: US/09/651,200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 325
; TYPE: PRT
; ORGANISM: sus sp.
US-09-651-200-20

Query Match 55.0%; Score 953; DB 4; Length 325;

Best Local Similarity 61.4%; Pred. No. 3.7e-81;

Matches 202; Conservative 44; Mismatches 73; Indels 10; Gaps 8;

Qy 7 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQFANSONOSLSLVFWQDOENLVLN 66
Db 1 MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQFANSONOSLSLVFWQDOENLVLN 60
Qy 67 EYVLGKEKFDSDVHSGYMGRTSFDSDWTLRLHNLQIKDGLYQCIILHHKFTGMIRHQ 126
Db 61 ELYRGOEKPHNYSKMGRTSFDSDWTLRLHNLQIKDGLYQCIILHHKFTGMIRHQ 120
Qy 127 NSELVLANFSPQEIPIVPSNITENVYINLTCSSIHGYPEPKKMSVLLRTKNSITIEYDGM 186
Db 121 SSDLSILANFSPQEIPIVPSNITENVYINLTCSSIHGYPEPKKMSVLLRTKNSITIEYDGM 180
Qy 187 QKSDQNVTELYDVSISLVSFPDVTNSMTIFCILETKRLSSPFSIELEDP-QPP- 242
Db 181 KKSQNNITELYNYSIRVSLPIPET-NVSIYCVLQLEPSKTLFLSLPCNIDAKPPVQPPV 239
Qy 243 PDHPIWITAVLPT-VIIICVMVFCILILMKKKKPRNSYKCGTNTMERESQTKKREK 300
Db 240 PDHILWIAALLVWLILCGWVFLTLRK-RKKQPGPSHECETIKRKERKESQTKNERVP 298
Qy 301 IHIPERSDEAQRVFKSKTSSTSSCDKSCF 329
Db 299 VH--ERSDDAQCVNMLKTAGSDNSTTDF 325

RESULT 13

US-09-651-200-18
; Sequence 18, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-562 (CIPA-62)
; CURRENT APPLICATION NUMBER: US/09/651,200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Felis catus
US-09-651-200-18

Query Match 52.1%; Score 903; DB 4; Length 329;

Best Local Similarity 58.5%; Pred. No. 1.8e-76;

Matches 190; Conservative 44; Mismatches 83; Indels 8; Gaps 7;

Qy 6 TMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQFANSONOSLSLVFWQDOENLVL 65
Db 7 TMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQFANSONOSLSLVFWQDOENLVL 66
Qy 66 NEVYLGEKFDSDVHSGYMGRTSFDSDWTLRLHNLQIKDGLYQCIILHHKFTGMIRHQ 125
Db 67 YEIPRGKPNQVHLKYGRTSFDKDNWTLRLHNLQIKDGLYQCIILHHKFTGMIRHQ 126
Qy 126 MNSLSVLANFSPQEIPIVPSNITENVYINLTCSSIHGYPEPKKMSVLLRTKNSITIEYDGM 184
Db 127 MSSDLSVLANFSPQEIPIVPSNITENVYINLTCSSIHGYPEPKKMSVLLRTKNSITIEYDGM 186
Qy 185 IMOKSDQNVTELYDVSISLVSFPDVTNSMTIFCILETKRLSSPFSIELE-DPOP 241
Db 187 VMKKSQNNVTLYNYSIRVSLPIPET-AHNVSVFCLKLETLMLSLPNDIAQPKDKDP 245
Qy 242 PDHPIWITAVLPT-VIIICVMVFCILILMKKKKPRNSYKCGTNTMERESQTKKREK 300
Db 246 EQGHFLWIAALLVWLILCGWVFLTLRK-RKKQPGPSHECETIKRKERKESQTKNERVP 304
Qy 301 IHIPERSDEAQRVFKSKTSSTSSCDKSCF 325
Db 305 YHVPERSDEAQC-VNMLKTAGSDKN 328

RESULT 14

US-08-456-104-4
; Sequence 4, Application US/08456104
; Patent No. 5861310
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,104
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-456-104-4

Query Match 42.9%; Score 743.5; DB 2; Length 309;
Best Local Similarity 51.5%; Pred. No. 1.3e-61;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;
QY 1 MDPQCTMGLSNILFYMAFLLSGAAPLKIQAYFNETADLPFCQFANSQNSLSLVVFWQDQ 60
DB 1 MDPRCTMGLAILFVTVLLISDAVSVETQAYFNGTAYLPCPFTKAQNISLSLVVFWQDQ 60
QY 61 ENLVNEVYLGEKEDSVHSKMGRTSFDSDSWTLRLHNLQIKDGLYQCIIHHKKEPTGM 120
DB 61 QKLVLYEHLGTEKLDVSNKYLGRTSFDRNNWTLRLHNVQIKDGSYDCFIQKKPTGS 120
QY 121 IRIHQMSLSLVANFSQPEIVPISNITENVYINLTCSIHGYPEPKKMSVLLRTKNSTI 180
DB 121 IILQQLTSLSVIANFSPEIKLAQNVGTGNSGINTCTSKQGHKPKKMYFLI--TNSTN 178
QY 181 EYDGMOKSDQNVTELYDVSLSVSPDVTNMTIFCILETDKTRLLSSPFSIELEDPO 240
DB 179 EYGDNMQISQDNVTELSLSLSLSPDGVHMTVVCVLETESNMKISSKPLNFTQEPFS 238
QY 241 PPPDHIPW--ITAVLPTVVICVMVFCILILMKWKKKRRPNRSYKCGTNTMEREESEQTKR 298
DB 239 P---QTYWKEITASVTALLVML--LIIVCHKKPNQPSRP-----SNTASKLERDSNADR 289
QY 299 EKHIPE 305
DB 290 ETINLKE 296

RESULT 15
US-08-479-744A-23
Sequence 23, Application US/08479744A
Patent No. 6084067
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,744A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-744A-23
Query Match 42.9%; Score 743.5; DB 3; Length 309;
Best Local Similarity 51.5%; Pred. No. 1.3e-61;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;
QY 1 MDPQCTMGLSNILFYMAFLLSGAAPLKIQAYFNETADLPFCQFANSQNSLSLVVFWQDQ 60
DB 1 MDPRCTMGLAILFVTVLLISDAVSVETQAYFNGTAYLPCPFTKAQNISLSLVVFWQDQ 60
QY 61 ENLVNEVYLGEKEDSVHSKMGRTSFDSDSWTLRLHNLQIKDGLYQCIIHHKKEPTGM 120
DB 61 QKLVLYEHLGTEKLDVSNKYLGRTSFDRNNWTLRLHNVQIKDGSYDCFIQKKPTGS 120
QY 121 IRIHQMSLSLVANFSQPEIVPISNITENVYINLTCSIHGYPEPKKMSVLLRTKNSTI 180
DB 121 IILQQLTSLSVIANFSPEIKLAQNVGTGNSGINTCTSKQGHKPKKMYFLI--TNSTN 178
QY 181 EYDGMOKSDQNVTELYDVSLSVSPDVTNMTIFCILETDKTRLLSSPFSIELEDPO 240
DB 179 EYGDNMQISQDNVTELSLSLSLSPDGVHMTVVCVLETESNMKISSKPLNFTQEPFS 238
QY 241 PPPDHIPW--ITAVLPTVVICVMVFCILILMKWKKKRRPNRSYKCGTNTMEREESEQTKR 298
DB 239 P---QTYWKEITASVTALLVML--LIIVCHKKPNQPSRP-----SNTASKLERDSNADR 289
QY 299 EKHIPE 305
DB 290 ETINLKE 296

Search completed: February 13, 2003, 11:33:51
Job time : 14.8918 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 11:29:24 ; Search time 14.5298 Seconds
(without alignments)
2044.459 Million cell updates/sec

Title: US-09-425-516-23

Perfect score: 1599

Sequence: 1 MDPRCTMGLAILFVTVLLI.....ETINLKELEPQIASAKPNAE 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1599	100.0	309	2 149522	gene B7-2 protein
2	743.5	46.5	329	1 A48754	B7-2 antigen - hum
3	700.5	43.8	330	2 146691	CD86 precursor - r
4	664	41.5	275	2 JC7604	CD86 spliced varia
5	231	14.4	309	2 149503	B-lymphocyte activ
6	223	13.9	321	2 154766	B-lymphocyte activ
7	206.5	12.9	299	2 146690	CD80 precursor - r
8	161.5	10.1	288	2 A45803	B-cell-restricted
9	144.5	9.0	289	2 G00031	B7 protein - red-c
10	144	9.0	365	2 JC7780	coxsackie- and ade
11	129.5	8.1	478	2 153960	PRR2 alpha - human
12	129.5	8.1	526	2 S70587	butyrophilin precu
13	129.5	8.1	538	2 168093	PRR2 delta - human
14	129.5	8.1	569	2 A46462	T cell activation
15	129	8.1	526	2 A37821	butyrophilin - bov
16	123	7.7	335	2 S58892	signaling lymphocy
17	121.5	7.6	1880	2 T18531	tractin - medicina
18	116	7.3	274	2 A47639	OX-2 membrane gly
19	114	7.1	487	2 S65133	butyrophilin - mou
20	113.5	7.1	391	2 T09058	butyrophilin homol
21	110	6.9	234	2 S01320	Ig kappa chain pre
22	110	6.9	1011	2 T13659	neuromusculin - fr
23	109.5	6.8	960	1 JN0677	protein-tyrosine k
24	106.5	6.7	518	2 JC4024	poliovirus recepto
25	106.5	6.7	761	1 TJHUNG	neural cell adhesi
26	106.5	6.7	974	1 A49714	protein-tyrosine k
27	105.5	6.6	219	2 S52028	Ig kappa chain - m
28	105.5	6.6	978	2 S16385	macrophage colony-
29	105	6.6	647	2 B41288	vascular cell adhe

30 104.5 6.5 299 2 S56749 junctional adhesio
31 104.5 6.5 806 2 A35963 protein-tyrosine k
32 103.5 6.5 219 2 PC4203 Ig kappa chain (mo
33 103.5 6.5 240 2 JL0143 antigen BCM1 precu
34 103 6.4 490 2 H70103 hypothetical prote
35 103 6.4 999 2 J38547 novel cellular pro
36 101.5 6.3 509 2 JC5288 SHP substrate-1 pr
37 101.5 6.3 513 2 JC5289 SHP substrate-1 pr
38 101 6.3 646 2 I38049 cell surface glyco
39 100.5 6.3 416 2 A54017 colon carcinoma-as
40 100.5 6.3 670 2 H96707 probable receptor
41 100 6.3 235 2 S20000 Ig light chain pre
42 100 6.3 526 1 A32164 biliary glycoprote
43 100 6.3 822 2 S19947 fibroblast growth
44 100 6.3 822 2 B49151 fibroblast growth
45 100 6.3 853 1 IJBONC neural cell adhesi

ALIGNMENTS

RESULT 1
I49522
gene B7-2 protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
R:Freeman, G.J.; Borriello, F.; Hodes, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim, J. Exp. Med. 178, 2185-2192, 1993
A:Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell pr
A:Reference number: I49522; MUID:94065585; PMID:7504059
A:Accession: I49522
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-309 <RES>
A:Cross-references: GB:I25606; NID:9432478; PIDN:AAA79770.1; PID:9432479
C:Genetics:
A:Gene: B7-2
C:Superfamily: B7-2 antigen

Query Match 100.0%; Score 1599; DB 2; Length 309;
Best Local Similarity 100.0%; Pred No 2.7e-114;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPRCTMGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLVWFQDQ 60
DB 1 MDPRCTMGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLVWFQDQ 60
QY 61 OKLVLYEHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGS 120
DB 61 OKLVLYEHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGS 120
QY 121 IILQOTLTSLSVIANFSEPEIKLAQNVGNSGINLTCTSKQGHKPKMYFLITNSTNEY 180
DB 121 IILQOTLTSLSVIANFSEPEIKLAQNVGNSGINLTCTSKQGHKPKMYFLITNSTNEY 180
QY 181 GDNMQISODNVTELFSTNSLSLSRFPDGVHMTVVCVLETESMKISSKPLNFTQFPSPQ 240
DB 181 GDNMQISODNVTELFSTNSLSLSRFPDGVHMTVVCVLETESMKISSKPLNFTQFPSPQ 240
QY 241 TYWKEITASVTVALLLVMLLIIVCHKKPNQSPRSNTASKLERSDNADRETINLKELEPQ 300
DB 241 TYWKEITASVTVALLLVMLLIIVCHKKPNQSPRSNTASKLERSDNADRETINLKELEPQ 300
QY 301 IASAKPNAE 309
DB 301 IASAKPNAE 309

RESULT 2
A48754
B7-2 antigen - human
N:Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor

```
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A48754; S39055
R;Freeman, G.J.; Gribben, J.G.; Boussiotis, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombard,
Science 262, 909-911, 1993
A;Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell proliferation
A;Reference number: A48754; MUID:94053735; PMID:7694363
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-329 <R>
A;Cross-references: GB:L45259; NID:9416368; PIDN:AAA58389.1; PID:9416369
A;Note: It is uncertain whether Met-1 or Met-2 is the initiator
R;Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somoza, C.
Nature 366, 76-79, 1993
A;Title: B70 antigen is a second ligand for CTLA-4 and CD28.
A;Reference number: S39055; MUID:94050123; PMID:7694153
A;Accession: S39055
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 7-329 <AZU>
A;Cross-references: GB:U04343; NID:9439838; PIDN:AAB03814.1; PID:9439839
C;Genetics:
A;Gene: GDB:CD86; CD28LG2
A;Cross-references: GDB:433597; OMIM:601020
A;Map position: 3q13.3-3q21
C;Superfamily: B7-2 antigen
C;Keywords: glycoprotein

Query Match 46.5%; Score 743.5; DB 1; Length 329;
Best Local Similarity 51.5%; Pred. No. 3.5e-49;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

QY 1 MDPRCTMGLAILFVTVLLISDAVSQVETQAYFNGTAYLPCPFTKAQNISLSLVVFWQDQ 60
DB 1 MDPCTMGSLNLFVWALLSGAAPLKIQAIFNETADLPQFANSQNSLSLVVFWQDQ 60
QY 61 QKLVLYEHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKPPGTS 120
DB 61 ENLVLYEVLGKEKFDVSHSKYMGRTSFDSWTLRLNLQIKDKGLYQCIHHKKPTGM 120
QY 121 IILQOQLTELVSIVANFSEPEIKLAQNVGTSGINLTCTSKQGHKPKKMYFLI--TNSTN 178
DB 121 IRIHQNSLSVLANSFQPEIVPISNITENVYINLTCSHIGYPPKPKMSVLLRTKNSTI 180
QY 179 EYGDNMQISQDNVTELFSSISLSLSPDGVWMTVVCVLETESMKISSKPLNFTQEPFS 238
DB 181 EYDGMQKSDQNVTELYDVSISLSVSPDVTNNITFCILETDKTRLLSSPFIETEDPQ 240
QY 239 P---QTYWKEITASVTALLVLM--LIIIVCHKPNQPSRP-----SNTASKLERDSNADR 289
DB 241 PPDPHPW--ITAVLPTVIICVMVFCULILWKWKKKRPNRSYKCGTNTMRESESEQTKKR 298
QY 290 ETINKLE 296
DB 299 EKIHIPE 305

RESULT 3
146691
CD86 precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 23-Jul-1999
C;Accession: I46691
R;Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule
A;Reference number: I46689; MUID:95369849; PMID:7642234
A;Accession: I46691
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-330 <ISO>
A;Cross-references: GB:D49842; NID:9755098; PIDN:BAA08642.1; PID:9755099
```

```
C;Superfamily: B7-2 antigen

Query Match 43.8%; Score 700.5; DB 2; Length 330;
Best Local Similarity 46.1%; Pred. No. 6.6e-46;
Matches 146; Conservative 58; Mismatches 94; Indels 19; Gaps 4;

QY 1 MDPRCTMGLAILFVTVLLISDAVSQVETQAYFNGTAYLPCPFTKAQNISLSLVVFWQDQ 60
DB 1 MDAGCTMGLSVTVFWALLSGAASLRIQAYFNKTADLPQCFNQSQRSLSELVFWQDQ 60
QY 61 QKLVLYEHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKPPGTS 120
DB 61 ERLVLYELFELGREGKPNVDPKYIGRTSFDSQWNLQHLNVOIKDGVYQCQFVHHRGAKGL 120
QY 121 IILQOQLTELVSIVANFSEPEIKLAQNVGTSGINLTCTSKQGHKPKKMYFLI--TNSTN 178
DB 121 VPIYQMSLSVLANSFQPEIVPISNITENVYINLTCSHIGYPPKPKMSVLLRTKNSTI 180
QY 179 EYGDNMQISQDNVTELFSSISLSLSPDGVWMTVVCVLETESMKISSKPLNFTQEPF- 237
DB 181 EYDGMQKSDQNVTELYDVSISLSVSPDVTNNITFCILETDKTRLLSSPFIETEDPQ 234
QY 238 -----SPQTYWKEITASVTALLVLM--LIIIVCHKPNQPSRPSTASKLERDSNADR 288
DB 235 VPADPVPVEKPRLWIAAVALTLIVVCGIVLFLTWKKEQEQPGVCECECTIKMDKAENEH 294
QY 289 RETINKLEPEQIASAK 305
DB 295 VEE-RVKIHEPEKIPAK 310

RESULT 4
JC7604
CD86 spliced variant CD86 deltaTM isoform - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C;Accession: JC7604
R;Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeannin, P.; Bonnefoy, J.Y.; Delneste, Y.
Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
A;Title: Identification of an alternatively spliced variant of human CD86 mRNA.
A;Reference number: JC7604; MUID:21092744; PMID:11162656
A;Accession: JC7604
A;Molecule type: mRNA
A;Residues: 1-275 <WAG>
C;Comment: This CD86 variant expressed by activated human monocytes, is a costimulatory.
C;Genetics:
A;Gene: cd86deltaTM
C;Keywords: immune response

Query Match 41.5%; Score 664; DB 2; Length 275;
Best Local Similarity 55.9%; Pred. No. 3.1e-43;
Matches 137; Conservative 34; Mismatches 68; Indels 6; Gaps 2;

QY 7 MGLAILFVTVLLISDAVSQVETQAYFNGTAYLPCPFTKAQNISLSLVVFWQDQKLVLY 66
DB 1 MGLSNILFVWAFLLSGAAPLKIQAIFNETADLPQFANSQNSLSLVVFWQDQENLVN 60
QY 67 EHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKPPGTSIILOOT 126
DB 61 EYVLGKEKFDVSHSKYMGRTSFDSWTLRLNLQIKDKGLYQCIHHKKPKGMRIRHQM 120
QY 127 LTELVSIVANFSEPEIKLAQNVGTSGINLTCTSKQGHKPKKMYFLI--TNSTNEYGDNM 184
DB 121 NSELVLANFSQPEIVPISNITENVYINLTCSHIGYPPKPKMSVLLRTKNSTIYDGM 180
QY 185 QISQDNVTELFSSISLSLSPDGVWMTVVCVLETESMKISSKPL-----NFTQEPSPQ 240
DB 181 QKSDQNVTELYDVSISLSVSPDVTNNITFCILETDKTRLLSSPFIETEDPQ 240
QY 241 TYWKE 245
DB 241 TKKRE 245
```


Db 119 KN-ENGSRFRHLTSVLTSTRADPPVPSI-----TDIGHDPNVKIRCSAGGFPEPRLA 173
QY 170 YFLITNSTNEYGD-----NMQISQDNVTFLFSISNLSLSPFDGVMHMTVVCVLETESMK 224
Db 174 WM-----EDGEELNAVNTTVDLDTELYSVSSSELDFTNVTN---NHSIVCLIKYGLS 223
QY 225 IS-----SKPLNFTQEPSPQ-TYWKETASVTVALLLVMLLIIVCHKKFNQSPRSNTA 278
Db 224 VSQIPFWKSP---KQEPPIQDLPFWIIPVSGALVLTAVLYCLACRH-----V 269
QY 279 SKLERDSNADRETINLKELEP 299
Db 270 ARWKR-TRNEETVGTERTLSP 289

RESULT 8
A45803
B-cell-restricted antigen B7 precursor - human
N:Alternate names: B-lymphocyte activation antigen B7
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999
C:Accession: I54495; A45803
R:Selvakumar, A.; Mohanraj, B.K.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.
Immunogenetics 36, 175-181, 1992
A:Title: Genomic organization and chromosomal location of the human gene encoding the B-
A:Reference number: I54495; MUID:92307753; PMID:1377173
A:Accession: I54495
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-288 <RES>
A:Cross-references: GB:M3077; NID:gi179327; PIDN:AAA58390.1; PID:gi179329
J. Freeman, G.J.; Freedman, A.S.; Segil, J.M.; Lee, G.; Whitman, J.F.; Nadler, L.M.
R. Immunol. 143, 2714-2722, 1989
A:Title: B7, a new member of the Ig superfamily with unique expression on activated and
A:Reference number: A45803; MUID:90010147; PMID:2794510
A:Accession: A45803
A:Molecule type: mRNA
A:Residues: 1-288 <PRE>
A:Cross-references: GB:M27533; NID:gi184680; PIDN:AAA36045.1; PID:g306916
C:Genetics:
A:Gene: GDB:CD80; CD28LG1; CD28
A:Cross-references: GDB:251792; OMIM:112203
A:Map position: 3q13.3-3q21
A:Introns: 34/1; 140/1; 234/1; 266/1
C:Superfamily: B-lymphocyte restricted antigen B7
C:Keywords: transmembrane protein
F:1-26/Domain: signal sequence #status predicted <SIG>
F:248-264/Domain: transmembrane #status predicted <TM>

Query Match 10.1%; Score 161.5; DB 2; Length 288;
Best Local Similarity 24.1%; Pred. No. 5.6e-05;
Matches 57; Conservative 51; Mismatches 100; Indels 29; Gaps 11;
QY 36 AYLPCTPTKAONISLSSELV---VFWDQOQKLVLYEHYLGTEKLDSDVN--AKYLGRTSFD- 89
Db 46 ATLSC-----GHNVSVEBLAQTRIYQKQKKNVL-----TWISGDMNIWPEYKNTIFDI 95
QY 90 RNNWTLRLHNVOIKDMGSDYDCFIQKPPPTGSIILQOQLTE--LSVIANFSEPEIKLAQNV 147
Db 96 TNNLSIVILALRPSDEGTVECVVLKYEK--DAFKREHLAEVTLVSVKADPPTPSISDFEIP 153
QY 148 TNGSGINLTCTSKQGHKPKKMYFLITNSTNEYDNQMOISQDNVTFLFSISNLSLSPFD 207
Db 154 TSNIR-RIICSTGGGPFPEHLSW--LENGELNAINTTVSQDPETELIYAVSSKLDFTNM-- 208
QY 208 GVMHMTVVCVLETESMKISSKPLNFTQEPSPQTYWKETASVTVALLLVMLLIIVC 264
Db 209 -TTNHSFVCLIKYGLHVRNQ--TFNWNTPKQEHFPDNLPSWAILTISVNGIFVIC 261

RESULT 9
G00031

B7 protein - fed-crowned mangabey (fragment)

C:Species: Cercopithecus torquatus (red-crowned mangabey, white-collared mangabey)
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 29-Sep-1999
C:Accession: G00031
R:Villinger, F.J.
submitted to the EMBL Data Library, January 1995
A:Reference number: G00217
A:Accession: G00031
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-289 <VII>
A:Cross-references: EMBL:U19833; NID:g644783; PIDN:AAA86700.1; PID:g644784
C:Genetics:
A:Gene: B7
C:Superfamily: B-lymphocyte restricted antigen B7
Query Match 9.0%; Score 144.5; DB 2; Length 289;
Best Local Similarity 23.6%; Pred. No. 0.0011;
Matches 56; Conservative 51; Mismatches 101; Indels 29; Gaps 11;
QY 36 AYLPCTPTKAONISLSSELV---VFWDQOQKLVLYEHYLGTEKLDSDVN--AKYLGRTSFD- 89
Db 46 ATLSC-----GHNVSVEBLAQTRIYQKQKKNVL-----TWISGDMNIWPEYKNTIFDI 95
QY 90 RNNWTLRLHNVOIKDMGSDYDCFIQKPPPTGSIILQOQLTE--LSVIANFSEPEIKLAQNV 147
Db 96 TNNLSIVILALRPSDEGTVECVVLKYEK--DAFKREHLAEVTLVSVKADPPTPSITDFEIP 153
QY 148 TNGSGINLTCTSKQGHKPKKMYFLITNSTNEYDNQMOISQDNVTFLFSISNLSLSPFD 207
Db 154 PSNIR-RIICSTGGGPFPEHLSW--LENGELNAINTTVSQDPETELIYVSSKLDFTNM-- 208
QY 208 GVMHMTVVCVLETESMKISSKPLNFTQEPSPQTYWKETASVTVALLLVMLLIIVC 264
Db 209 -TTNHSFVCLIKYGLHVRNQ--TFNWNTPKQEHFPDNLPSWAILTISVNGIFVIC 261

RESULT 10

JC7780

coxackie- and adenovirus receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002

C:Accession: JC7780

R:Thoenen, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.

Biochem. Biophys. Res. Commun. 288, 805-808, 2001

A:Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus recept.

A:Reference number: JC7780

A:Contents: Liver

A:Accession: JC7780

A:Molecule type: mRNA

A:Residues: 1-365 <THO>

A:Cross-references: GB:AY033651

C:Comment: This protein serves as the primary adenoviral attachment site on bovine cell.

Query Match 9.0%; Score 144; DB 2; Length 365;
Best Local Similarity 23.2%; Pred. No. 0.0016;
Matches 64; Conservative 47; Mismatches 117; Indels 48; Gaps 14;

QY 35 TAYLPCTPTKAONISLSSELVFW---ODQOK---LVLVEHYLGTEKLDSDVNAKVLGRT 86
Db 36 TAYLPCKTFLGPE-DQGPDLIELWLSPADNOKVDVILYS---GDKIYDDYYQDLKGRV 91
QY 87 SFDNRN-----TLRLHNVOIKDMGSDYDCFIQKPPPTGSIILQOQLTELSVIANFSEPE 140
Db 92 HTSNDLKSQDASINVTNLQSLDIGTYQCKVKAPGVGNKKIQLTVLVKPSGIRCVDGS 151
QY 141 IKLAQNVTCNSGINLTCTSKQGHKPKKMYFLITNSTNEYDNQMOISQDNVTFLFSISNS 200
Db 152 EBI-----GND-FKLKCEPKGS-----LPIRYEWOXKLSQKLTSLWPEW--TSPV 196
QY 201 LSLSPFDGVMHMTVVCVLETESMKISSKPLNFTQEPSPQTYWKETASV---TVALLIV 257
Db 197 ISVKNAEASGYTCTVRN---RVGSDQCLLRDLVDPSPNRRAGTIAGAVIGTLLALVLI 253

R:Wang, P.L.; O'Farrell, S.; Clayberger, C.; Krensky, A.M.
J. Immunol. 148, 2600-2608, 1992
A:Title: Identification and molecular cloning of tactile. A novel human T cell activation
A:Reference number: A46462; MUID:92218864; PMID:1313846
A:Accession: A46462
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-569 <WAN>
A:Cross-references: GB:M88282; NID:g338671; PIDN:AAA36662.1; PID:g338672
A>Note: sequence extracted from NCBI backbone (NCBI:94434, NCBI:94435)
C:Keywords: transmembrane protein

Query Match 8.1%; Score 129.5; DB 2; Length 569;
Best Local Similarity 24.4%; Pred. No. 0.037;
Matches 77; Conservative 40; Mismatches 117; Indels 81; Gaps 15;
QY 18 LLISDAVSVE-----TQAYFNGTAVLPCFPTKAQNISLSLVVFWQ-----DQOKLVL 65
DB 134 LLIQTHVTADENSNHTIEINQTLTLEIPCQFQNSKIS-SEFTYAMSVEDNGTQETLIS 192
QY 66 YEHVLGTEKLDVSNAYKLGRTSFDNNWTLRLHNVOKDMG-SYDCFIQKKPPTGSIILQ 124
DB 193 QNHLSNSTLLKDRVK-LG-----TYRLHLSFVQIFDGRKFSCHIRVGP-----N 238
QY 125 QTLTSLVIANFSEPEIKLAQNVGNGINL-----TCTSKQGHKPKKMYFLITNSTNE 179
DB 239 KILRSSTTVKFAKPEIPVI--VENNSTDVLVERRFTCLLKNVFPKANITWFDIGSFLHD 296
QY 180 YGDNNOQIS-----QDNVTELFPSI-----SNSLSLSPDGVVHMTVVCVLETESMKISSK 228
DB 297 EKEGIYITNEERKGDGFLKLSVLTVRHNSKPAQSDNLTICWMAISFVGNKVMNISSE 356
QY 229 PLNF-----TQEPF-----SPQTYWKEITASVTVALLLVMLLIIV 263
DB 357 KITFLGSEISSDPLSVTSTLTDTQSPASSVSPARY--PATSSVT-----LVDV 406
QY 264 CHKKNQPSRPSNTA 278
DB 407 SALRPNTTPQPSNSS 421

RESULT 15

A37821
butyrophilin - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 05-Nov-1999
C:Accession: A37821
R:Jack, L.J.W.; Mather, I.H.
J. Biol. Chem. 265, 14481-14486, 1990
A:Title: Cloning and analysis of cDNA encoding bovine butyrophilin, an apical glycoprotein
A:Reference number: A37821; MUID:90354441; PMID:2387867
A:Accession: A37821
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-526 <JAC>
A:Cross-references: GB:M3551; NID:g1763685; PIDN:AAB39766.1; PID:g162773
C:Keywords: transmembrane protein

Query Match 8.1%; Score 129; DB 2; Length 526;
Best Local Similarity 21.7%; Pred. No. 0.036;
Matches 73; Conservative 60; Mismatches 139; Indels 64; Gaps 15;
QY 3 PRCWTGLAIIIFVTLLIS-----DAVSVEIQ--AFNGTAYLPCFPPTKAQNISLSLV 54
DB 5 PNSCLAGCLLIIFILLQPKLDSAPDVIQGPFLAVGVGDAELFCRL--SPNVSAKME 62
QY 55 VFW-QDOOKLVLYEHLGTEKLDVSNAYKLGRTS-----FDRNWTLLHNVQIKMGYSY 108
DB 63 LRWFRKVSAPFVSRGEGEAEYRGRVSLVEDHIAEGSVAVRIQEVKASDDGEY 122
QY 109 DCFIQKKPPTGSIILQOQTLTSLVIANFSEPEIKLAQNVGNGINLTCTSKQGHKPKK 168

DB 123 RCFRQDEN-----YEEAIVHLKVAALGSDPHISMKVQESGE--IQLECTSVGVWYPEPO- 174
QY 169 MYFLITNSTNEYGDNMOISQDNVTELPFISNSISLSFPD--GVVHMTVVCVLETESMKIS 226
DB 175 -----VQWRTHRGEEFPMSERN---PDEGLFTVRASVLIINDSSMKNV 216
QY 227 S---KPLNFTQ-----EPSPQTYWKEITA-SVTVALLLVMLLI-----VCHKKP 268
DB 217 SCCIRNLLLGQEKQVEVSIPASFPPLTPMVAVALVWLGLLTIGSIFFTWRLYKERS 276
QY 269 NQPSRESNTASKLERDSNADRETINLKE--LEPOIA 302
DB 277 RQRNEFSKELLEEKLKWKRAIHLHAVDTLDPDTA 312

Search completed: February 13, 2003, 11:33:22
Job time : 16.5298 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 11:23:59 ; Search time 16.4671 Seconds
(without alignments)
778.291 Million cell updates/sec

Title: US-09-425-516-23

Perfect score: 1599

Sequence: 1 MDPRTGMLAILFVTVLLI.....ETINKELEPQIASAKPNAE 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1599	100.0	309	1	CD86 MOUSE
2	743.5	46.5	329	1	CD86 HUMAN
3	700.5	43.8	330	1	CD86 RABIT
4	227.5	14.2	306	1	CD80 MOUSE
5	206.5	12.9	299	1	CD80 RABIT
6	182	11.4	302	1	ICOL HUMAN
7	175	10.9	322	1	ICOL MOUSE
8	161.5	10.1	288	1	CD80 HUMAN
9	146	9.1	319	1	A33 HUMAN
10	129.5	8.1	343	1	SLAM MOUSE
11	129.5	8.1	526	1	BUTY HUMAN
12	129.5	8.1	538	1	PVR2 HUMAN
13	129.5	8.1	569	1	TACT HUMAN
14	129	8.1	526	1	BUTY BOVIN
15	127.5	8.0	298	1	JAM2 HUMAN
16	123	7.7	335	1	SLAM HUMAN
17	120	7.5	298	1	JAM1 BOVIN
18	120	7.5	524	1	BUTY MOUSE
19	117	7.3	365	1	CXAR HUMAN
20	116	7.3	274	1	OX2G HUMAN
21	115	7.2	365	1	CXAR MOUSE
22	111	6.9	517	1	PVR1 HUMAN
23	109.5	6.8	977	1	KIT CHICK
24	108.5	6.8	960	1	JAM1 MOUSE
25	108	6.8	457	1	CD4 SAISC
26	106.5	6.7	761	1	NCA2 HUMAN
27	106.5	6.7	848	1	NCA1 HUMAN
28	106	6.6	515	1	PVR1 MOUSE
29	105.5	6.6	977	1	KFNS MOUSE
30	105.5	6.6	978	1	KFNS RAT
31	104.5	6.5	299	1	JAM1 HUMAN
32	104.5	6.5	806	1	CEK2 CHICK
33	104	6.5	515	1	PVR1_PIG

34	103.5	6.5	240	1	CD48 MOUSE
35	103	6.4	490	1	Y032 BORBU
36	103	6.4	999	1	MERK_HUMAN
37	101	6.3	646	1	MU18_HUMAN
38	100	6.3	348	1	KILO RAT
39	100	6.3	526	1	CEA1_HUMAN
40	100	6.3	853	1	NCA1_BOVIN
41	99.5	6.2	417	1	PVR_HUMAN
42	99.5	6.2	823	1	CEK3 CHICK
43	99.5	6.2	847	1	CD22_HUMAN
44	99.5	6.2	994	1	MERK_MOUSE
45	99.5	6.2	994	1	MERK_RAT

P18181	mus musculus
O51063	borrelia bu
Q12866	homo sapien
P43121	homo sapien
Q920J8	rattus norv
P13688	homo sapien
P31836	bos taurus
P15151	homo sapien
P18461	gallus gall
P20273	homo sapien
O60805	mus musculus
P57097	rattus norv

ALIGNMENTS

RESULT 1

CD86 MOUSE	
ID_CD86_MOUSE	STANDARD; PRT; 309 AA.
AC P42082;	
DT 01-NOV-1995 (Rel. 32, Created)	
DT 01-NOV-1995 (Rel. 32, Last sequence update)	
DT 15-JUN-2002 (Rel. 41, Last annotation update)	
DE T lymphocyte activation antigen CD86 precursor (Activation B7-2	
DE antigen) (Early T cell costimulatory molecule-1) (ETC-1).	
GN CD86	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX NCBI_TaxID=10090;	
RN [1]	
RN SEQUENCE FROM N.A.	
RX MEDLINE=94065585; PubMed=7504059;	
RA Freeman G.J., Borriello F., Hodes R.J., Reiser H., Gribben J.G.,	
RA Ng J.W., Kim J., Goldberg J.M., Haticock K., Laszlo G., Lombard L.A.,	
RA Wang S., Gray G.S., Nadler L.M., Sharpe A.H.;	
RT "Murine B7-2, an alternative CTLA4 counter-receptor that costimulates	
RT T cell proliferation and interleukin 2 production."	
RL J. Exp. Med. 178:2185-2192(1993).	
RN [2]	
RN SEQUENCE FROM N.A.	
RC STRAIN=129;	
RX MEDLINE=96094437; PubMed=7499829;	
RA Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;	
RT "Differential expression of alternate mB7-2 transcripts."	
RL J. Immunol. 155:5490-5497(1995).	
RN [3]	
RN SEQUENCE OF 7-309 FROM N.A.	
RX MEDLINE=94230971; PubMed=7513726;	
RA Chen C., Gault A., Shen L., Nabavi N.;	
RT "Molecular cloning and expression of early T cell costimulatory	
RT molecule-1 and its characterization as B7-2 molecule."	
RL J. Immunol. 152:4929-4936(1994).	
CC -!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL	
CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY	
CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY	
CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,	
CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T	
CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.	
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.	
CC -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS.	
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.	
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.	
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.	
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-7 IS THE INITIATOR.	

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EMBL; L25259; AAA58389.1; .
EMBL; U04343; AAB03814.1; .
EMBL; U17722; AAA86473.1; .
EMBL; U17717; AAA86473.1; JOINED.
EMBL; U17718; AAA86473.1; JOINED.
EMBL; U17719; AAA86473.1; JOINED.
EMBL; U17721; AAA86473.1; JOINED.
EMBL; U17723; AAA86473.1; JOINED.
Genew; HGNC:1705; CD86.
MIM; 601020; .
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Immunoglobulin domain, T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 329 T LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT DOMAIN 24 247 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 248 268 POTENTIAL.
FT DOMAIN 269 329 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 117 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 150 225 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 40 110 POTENTIAL.
FT DISULFID 157 218 POTENTIAL.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 47 47 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 27 27 K -> E (IN REF. 3).
FT SEQUENCE 329 AA; 37696 MW; 65D4F3826889CF7D CRC64;
Query Match 46.5%; Score 743.5; DB 1; Length 329;
Best Local Similarity 51.5%; Pred. No. 4.3e-52;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;
QY 1 MDPRTMGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPFTKAQNTLSLSELVVFWDDQ 60
Db 1 MDPQTMGLSNILFVNAFLSGLAAPLKIQAYFNETADLPQCFANSQNSLSLSELVVFWDDQ 60
QY 61 QKLVLYEHYLGTEKLDVSNVAKYLGRTSPDRNNWTLRLHNVQIKDMGSDCFIQKKPPTGS 120
Db 61 ENLVLENYLGREKFDPSVHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKTGM 120
QY 121 ILLOQTLELTVANFSEPEIKLAQNVGTSGINLTCTSKQGHKPKKMYFLI--TNSTN 178
Db 121 IRIHQNSELSLANFSPQEIPIVSNITENYINLTCSIHGYPPEPKMSVLLRTKNSTI 180
QY 179 EYGDNMQISODNVTELFSTNSLSLSPDGVHMTVVCVLETESMKISKPLNFTQFPFS 238
Db 181 EYDGMQISODNVTELYDVSLSVSPDVTSNWTFCTILETKRLSSPFSFELEDPPQ 240
QY 239 P---QTYWKEITASVTVALLLVWL--LIIVCHKKPNQPSRP----SNTASKLERDSNADR 289
Db 241 PPPDHPWP--ITAVLPFTVIICVMYFCLILWKWKKRPRNSYKCGTNTMERESEQTKKR 298
QY 290 ETINLKE 296
Db 299 EKIHIPE 305
RESULT 3
CD86_RAB1
ID CD86_RAB1 STANDARD; PRT; 330 AA.
```

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AC P42071;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE B lymphocyte activation antigen CD86 precursor (Activation B7-2
DE antigen).
DE
DE
DE
GN CD86.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B/J X CHBB:HM;
RX MEDLINE=95369849; PubMed=7642234;
RA Isono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell
RT costimulatory molecules."
RL Immunogenetics 42:217-220(1995).
CC -!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION. BY
CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
CC SUCH AS DECIDING BETWEEN IMMUNITY AND ENERGY THAT IS MADE BY T
CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC -!- SUBCELLULAR LOCATION: type 1 membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).

EMBL; D49842; BAA08642.1; .
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 330 B LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT DOMAIN 23 247 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 248 268 POTENTIAL.
FT DOMAIN 269 330 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 117 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 150 225 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 40 110 POTENTIAL.
FT DISULFID 157 218 POTENTIAL.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 330 AA; 37142 MW; 935CDD65C57E3EE1 CRC64;
Query Match 43.8%; Score 700.5; DB 1; Length 330;
Best Local Similarity 46.1%; Pred. No. 1.1e-48;
Matches 146; Conservative 58; Mismatches 94; Indels 19; Gaps 4;



QY 1 MDPRTMGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPFTKAQNTLSLSELVVFWDDQ 60
Db 1 MDAGCTMGLSVTVFVMAALLSGLAASLRIQAYFNKTADLPQCFINSQSRSLSLSELVVFWDDQ 60
QY 61 QKLVLYEHYLGTEKLDVSNVAKYLGRTSPDRNNWTLRLHNVQIKDMGSDCFIQKKPPTGS 120


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Db 61 ERULVLELFGREKEDNDPPIKIGRTSFDQESWNQLQHNVIKDKGVYQCFVHHRGAKGL 120
Qy 121 ILIQOTLTSLSVIANFSEPEIKLAQNVTGNSGINLTCTSKQGHKPKKMYFLI--TNSYN 178
Db 121 VPIQWNSLSVLNFTQPEITLISNTRSAINLTSCSSVQGYPEPKKMPFVLKTNATT 180
Qy 179 EYGDNQISODNVNTELSLSLSPDGVHMTVVCVLETESMKISSKPLNFTQEPF- 237
Db 181 EYDGVIEKQDNVTGLYNISGISGIFSDIRNATYCVLQTESTE-----TYSQHFP 234
Qy 238 -----SPQYKKEITASVTALLVMLLIIVCHKPNQPSRPSNTASKLERSNAD 288
Db 235 VPADPVPVEKPLWIAAVALTLVVCVGLVFLTLWKRKKEQPGVCECETIKMDKAENEH 294
Qy 289 RETINLKELEPOIASAK 305
Db 295 VEE-RVKIHEPEKIPAK 310
RESULT 4
ID_CD80_MOUSE STANDARD; PRT; 306 AA.
AC OQ0609;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1
antigen) (B7).
GN CD80 OR B7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=91341422; PubMed=1714935;
RA Gray G.S., Freeman G.J., Glimi C.D., Lombard D.B., Zhou L.J.,
RA White M., Fingeroth J.D., Gribben J.G., Nadler L.M.;
RT "Structure, expression, and T cell costimulatory activity of the
RT murine homologue of the human B lymphocyte activation antigen B7.";
RL J. Exp. Med. 174:625-631(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=93307789; PubMed=7686531;
RA Selvakumar A., White P.C., Dupont B.;
RT "Genomic organization of the mouse B-lymphocyte activation antigen
RT B7.";
RL Immunogenetics 38:292-295(1993).
CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA
CC INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING B-CELL
CC MALIGNANCIES.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-
CC ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND
CC IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL; X60958; CAA43291.1; .
DR EMBL; L12589; AAA37240.1; ALT SEQ.
DR EMBL; L12585; AAA37240.1; JOINED.
DR EMBL; L12586; AAA37240.1; JOINED.
DR EMBL; L12587; AAA37240.1; JOINED.
DR EMBL; L12588; AAA37240.1; JOINED.
DR PIR; S17291; S17291.
DR HSP; P33681; 1DR9.
DR MGD; MGI:101775; Cd80.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; IG_Like; 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL 1 37
FT CHAIN 38 306
FT DOMAIN 38 246
FT TRANSMEM 247 268
FT DOMAIN 269 306
FT DOMAIN 47 126
FT DOMAIN 158 226
FT DOMAIN 227 246
FT DISULFID 54 119
FT DISULFID 165 219
FT CARBOHYD 93 93
FT CARBOHYD 99 99
FT CARBOHYD 149 149
FT CARBOHYD 189 189
FT CARBOHYD 210 210
FT CARBOHYD 214 214
SQ SEQUENCE 306 AA; 34589 MW; 1DBADE0931B84C62 CRC64;
Query Match 14.2%; Score 227.5; DB 1; Length 306;
Best Local Similarity 25.5%; Pred. No. 4.8e-11;
Matches 78; Conservative 58; Mismatches 127; Indels 43; Gaps 11;
Qy 11 ILIFVTLLISDA---VSVETQAYFNAGTAYILPCFPFTRKAQNISLSLVFWQDQOKLVLYE 67
Db 22 ILLFVLLIRLSQSSVDDEQLSKSVKDKVLLPCRYNSPHE-DESDRIYWKHKDVKVL-- 78
Qy 68 HVLGTEKLDVNA-----KYLGRTSFDNNWTLRLHNVIQIKDMGSDYCFQKPKPTGS 120
Db 79 -----SVIAGKLVKWPYKNTLYDNTYSLIILGLVLSDRGTYSVQKRGRTY 129
Qy 121 ILQOTLTSLSVIANFSEPEIKLAQNVTGNSGINLTCTSKQGHKPKKMYFLITNSTNEY 180
Db 130 EVKHLALVKLSIKADFTPNITESGNPSADTK-RIITCFASGGFPKPR--FSMLENGREL 186
Qy 181 GDNMQISODNVNTELSLSLSPDGVHMTVVCVLETESMKISSKPLNFTQEPF--- 237
Db 187 GINTTISQDPESELYTISQDLP---NTRNHTIKCLIKYGDHADVSE---DFTWEKPED 240
Qy 238 ---SPQ---YKKEITASVTALLVMLLIIVCHK---KPNQPSRPSNTASKLERSNAD 288
Db 241 PDSKNTLVLEAGFGAVITVVVVIKCFKHSRFRNEASRETNNSLTFGPEALA 300
Qy 289 RETINL 294
Db 301 EQTVEL 306
RESULT 5
ID_CD80_RABIT STANDARD; PRT; 299 AA.
AC P42070;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1

DE GN antigen).

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OK NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=B/J X CHBB:HM;

RA MEDLINE=95369849; PubMed=7642234;

RA Isono T., Seto A.;

RT "Cloning and sequencing of the rabbit gene encoding T-cell

RT costimulatory molecules.;"

RL Immunogenetics 42:217-220(1995).

CC -I- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T

CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE

CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS

CC RECEPTOR.

CC -I- SUBCELLULAR LOCATION: Type I membrane protein.

CC -I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

CC -I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

CC -I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

CC -----

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CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; D49843; BAA08643.1; --

DR HSSP; P33681; 1DR9.

DR InterPro; IPR003599; IG

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003800; IG_Like.

DR Pfam; PF00047; IG; 1.

DR SMART; SM00409; IG; 1.

DR SMART; SM00410; IG_Like; 1.

KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;

KW Receptor.

FT SIGNAL

FT CHAIN 1 32 POTENTIAL

FT CHAIN 33 299 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.

FT DOMAIN 33 243 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 244 264 POTENTIAL.

FT DOMAIN 265 299 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 42 122 IG-LIKE V-TYPE DOMAIN.

FT DOMAIN 154 222 IG-LIKE C2-TYPE DOMAIN.

FT DISULFID 49 115 POTENTIAL.

FT DISULFID 161 215 POTENTIAL.

FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 299 AA; 33513 MW; 67442235EC91DE0 CRC64;

Query Match 12.9%; Score 206.5; DB 1; Length 299;

Best Local Similarity 26.5%; Pred. No. 2.2e-09;

Matches 85; Conservative 58; Mismatches 111; Indels 67; Gaps 19;

Qy 3 PRCT-MGLAIIFFVTLISDAVSEVTOAYFNGTAVLPCTFKAGNISLSLSELV---VFWQ 58

Db 12 PRCLHLKCLLLAAGLHFGSGISQVTKS-VKEMAALSCDY-----NISIDELARMYIYWQ 66

Qy 59 DQKQVLYEHLVGTKEKLS-----VNAYKLGRTSFD-RNNWTLRLHNVQIKDMGSDYCPFIQ 113

Db 67 KDQQMWL-----SIISGQVEVWPEYKRNTPDIIINNLSLMLALRLSDKGTTCVWQ 118

Qy 114 KKPPTSGIILOQ-TUTELSVIANFSEPEIKLAQNVTVGNSGIN---LCTSKQGHKPKKW 169

Db 119 KN-ENGSRREHLTSVTLIRADFPVPSI-----TDIGHDPNVKIRCSASGGFPEPRLA 173

Qy 170 YFLTNTSTNEYGD-----NMQISQDNVTTELFSISLSLSFDPGVWHMTVCVLETSMK 224

Db 174 WM-----EDGEELNAVNTTVDQDLDTLSYSSSELDFTVNTN---NHSIVCLIKYGELS 223

Qy 225 IS-----SKPLNFTQFPSPQ-TYKKEITASVTVALLLVMLLIIVCHKKPKNPQSPSNTA 278

Db 224 VSQIFPWSKP---KQEPPIDQLPFWVIIPVSGALVLTAVVLYCLACRH-----V 269

Qy 279 SKLERSNADRETINKLELEP 299

Db 270 ARWKR-TRNEETVGTGERLSP 289

RESULT 6

ICOL HUMAN STANDARD; PRT; 302 AA.

ID ICOL HUMAN

AC 075144; Q9NRQ1; Q9HDI8;

DT 15-JUL-1999 (Rel. 38, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein GL50)

DE (B7-related protein-1) (B7RP-1).

GN ICOSL OR B7H2 OR B7RP1 OR KIAA0653.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OK NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Dendritic cell;

RX MEDLINE=20477846; PubMed=11023515;

RA Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;

RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds

RT ICOS.;"

RL Blood 96:2808-2813(2000).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.

RC TISSUE=Peripheral blood lymphocytes;

RX MEDLINE=20465019; PubMed=11007762;

RA Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K.,

RA Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H.,

RA Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;

RT "Characterization of a new human B7-related protein: B7RP-1 is the

RT ligand to the co-stimulatory protein ICOS.;"

RL Int. Immunol. 12:1439-1447(2000).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Leukocyte;

RX MEDLINE=20126021; PubMed=10657606;

RA Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,

RA Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,

RA Jacobs K.A., Collins M.;

RT "Identification of GL50, a novel B7-like protein that functionally

RT binds to ICOS receptor.;"

RL J. Immunol. 164:1653-1657(2000).

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=98403880; PubMed=9734811;

RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,

RA Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X.

RT The complete sequences of 100 new cDNA clones from brain which can

RT code for large proteins in vitro.;"

RL DNA Res. 5:169-176(1998).

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RP SEQUENCE FROM N.A. (ISOFORM 2).

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RX MEDLINE=98403880; PubMed=9734811;

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RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;

RX MEDLINE=98403880; PubMed=9734811;

RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,

RA Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X.

RT The complete sequences of 100 new cDNA clones from brain which can

RT code for large proteins in vitro.;"

RL DNA Res. 5:169-176(1998).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;

RX MEDLINE=98403880; PubMed=9734811;

RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,

RA Kotani H., Nomura N., Ohara O.;

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RT The complete sequences of 100 new cDNA clones from brain which can

RT code for large proteins in vitro.;"

RL DNA Res. 5:169-176(1998).

RN [5]

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RC TISSUE=Brain;

RX MEDLINE=98403880; PubMed=9734811;

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RA Kotani H., Nomura N., Ohara O.;

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RT code for large proteins in vitro.;"

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RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;

RX MEDLINE=98403880; PubMed=9734811;

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RX MEDLINE=98403880; PubMed=9734811;

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RA Kotani H., Nomura N., Ohara O.;

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RT The complete sequences of 100 new cDNA clones from brain which can

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RL DNA Res. 5:169-176(1998).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;

RX MEDLINE=98403880; PubMed=9734811;

RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,

RA Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X.

RT The complete sequences of 100 new cDNA clones from brain which can

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RL DNA Res. 5:169-176(1998).

RN [5]

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RC TISSUE=Brain;

RX MEDLINE=98403880; PubMed=9734811;

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RA Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X.

RT The complete sequences of 100 new cDNA clones from brain which can

RT code for large proteins in vitro.;"

RL DNA Res. 5:169-176(1998).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;

RX MEDLINE=98403880; PubMed=9734811;

RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,

RA Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X.

RT The complete sequences of 100 new cDNA clones from brain which can

RT code for large proteins in vitro.;"

RL DNA Res. 5:169-176(1998).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;

RX MEDLINE=98403880; PubMed=9734811;

RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,

RA Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X.

RT The complete sequences of 100 new cDNA clones from brain which can

RT code for large proteins in vitro.;"

RL DNA Res. 5:169-176(1998).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;

RX MEDLINE=98403880; PubMed=9734811;

RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,

RA Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X.

RT The complete sequences of 100 new cDNA clones from brain which can

RT code for large proteins in vitro.;"

RL DNA Res. 5:169-176(1998).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;

RX MEDLINE=98403880; PubMed=9734811;

RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,

RA Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X.

RT The complete sequences of 100 new cDNA clones from brain which can

RT code for large proteins in vitro.;"

RL DNA Res. 5:169-176(1998).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;

RX MEDLINE=98403880; PubMed=9734811;

RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,

RA Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X.

RT The complete sequences of 100 new cDNA clones from brain which can

CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
CC STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).
CC SUBCELLULAR LOCATION: Type 1 membrane protein (By similarity).
CC -!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,
CC KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE
CC MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES,
CC SPLEEN, THYMUS AND TONSIL). WHILE ISOFORM 2 IS DETECTED ONLY IN
CC LYMPH NODES, LEUKOCYTES AND SPLEEN.
CC -!- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY
CC TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND
CC MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- CAUTION: Ref.4 sequence differs from that shown in position 300
CC onward for an unknown reason.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; AF199028; AAF34739.1; -
CC ENBL; AF289028; AAG01176.1; -
CC ENBL; AF216749; AAK16241.1; -
CC ENBL; AX014553; BAA31628.1; ALT_SEQ.
CC ENBL; AX100595; CAC36465.1; -
CC MIM; 605717; -
CC InterPro: IPR003599; IG.
CC InterPro: IPR003006; IG_MHC.
CC InterPro: IPR003600; IG_like.
CC Pfam; PF00047; IG; 2.
CC SMART; SM00409; IG; 1.
CC SMART; SM00410; IG like; 1.
CC B-cell activation; Immune response; Glycoprotein;
CC Immunoglobulin domain; Signal; Transmembrane; Multigene family;
KW Alternative splicing.
KW SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 302 ICOS LIGAND.
FT DOMAIN 19 256 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 257 277 POTENTIAL.
FT DOMAIN 278 302 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 30 120 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 151 223 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 37 113 POTENTIAL.
FT DISULFID 158 216 POTENTIAL.
FT CARBOHYD 70 70 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 225 225 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 300 302 GHV -> ESWNLLLLLS (IN ISOFORM 2).
SQ SEQUENCE 302 AA; 33349 MW; 647934E21B55E34A CRC64;
Query Match 11.4%; Score 182; DB 1; Length 302;
Best Local Similarity 23.6%; Pred. No. 2e-07;
Matches 70; Conservative 61; Mismatches 117; Indels 48; Gaps 14;
QY 8 GLALIFETVLLSDAVSVETQAYENGATYLPCTPFTKAQNISLSLVVFWQ-DOQKLVLV 66
DB 7 GLLEFLSS--LRADTQKEVRMVGSDVELSCACPGSRFDLNDVYVWTSSKTVWT 64
QY 67 EHYLGTEKLDVSNVAKYLGRTSFD-----RNNWTLRLHNHVOIKDMSYDCFTQKXPTGSI 121

Db 65 YHFPQSSLENVDSRYNRALMSPAGMLRGDFSLRLEFNVTPQDEQKPHCLVLSQ-----SL 120
QY 122 ILQQTUT---ELSVIANSEPEIKLAQNVGTSGINLCTSKQGHKPKKMYFLITNSTN 178
Db 121 GFOEVLVSVEVTLHVAANFSVFWVS-APHSPSODELFTTCTTSINGYPRP-NVYWI--NKT- 175
QY 179 EYGDNMQISQD-----NVTELFISNSLSLSPFDGVMHMTVVVCVLET-----ESMKIS 226
Db 176 ---DNLSDQALQNDTVFLNWRGLYDVSVLRARTPSV---NIGCCIEVLLQONLTVG 229
QY 227 SKPLNTQE-----FSPQTYWKETASVTVALLVMLLI-----VCHKKPKQPS 272
Db 230 SQTGNDIGERDKITENPVSTGKNAATMSILAVLCULLVVVAIGWVCRDRCLOHS 285
RESULT 7
ID ICOL_MOUSE STANDARD; PRT; 322 AA.
AC Q9UJH8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein GL50)
DE (B7-related protein-1) (B7RP-1) (LICOS).
GN ICOSL OR B7H2 OR B7RP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Lymphocytes;
RX MEDLINE=2083495; PubMed=10617205;
RA Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,
RA Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Rafuri-Bladt A.,
RA Brankow D., Campbell P., Chang D., Chiu L., Dai T., Duncan G.,
RA Elliott G.S., Hui A., McCabe S.M., Scully S., Shahinian A.,
RA Shaklee C.L., Van G., Mak T.W., Senaldi G.;
RT "T-cell co-stimulation through B7RP-1 and ICOS";
RL Nature 402:827-832(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Thymus;
RX MEDLINE=20015817; PubMed=10549624;
RA Swallow M.M., Wallin J.J., Sha W.C.;
RT "B7h, a novel costimulatory homolog of B7.1 and B7.2, is induced by
RT TNFalpha";
RL Immunity 11:423-432(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C3H/HeJ; TISSUE=Fetal thymus;
RX MEDLINE=20126021; PubMed=10657606;
RA Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,
RA Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,
RA Jacobs K.A., Collins M.;
RT "Identification of GL50, a novel B7-like protein that functionally
RT binds to ICOS receptor.";
RL J. Immunol. 164:1653-1657(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Periphera blood lymphocytes;
RX MEDLINE=21286479; PubMed=11390480;
RA Ling V., Wu P.W., Miyashiro J.S., Marusic S., Finnerty H.F.,
RA Collins M.;
RT "Differential expression of inducible costimulator-ligand splice
RT variants: lymphoid regulation of mouse gl50-b and human gl50
RT molecules.";
RL J. Immunol. 166:7300-7308(2001).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Ling V., Dunussi-Joannopolulos K.;
RT "Gl50 molecules and uses therefor.";

RT cell proliferation, cytokine production, and generation of CTL.";
 RL J. Immunol. 154:97-105(1995).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 35-234.
 RX MEDLINE=40125021; PubMed=10661405;
 RA Ikemizu S., Gilbert R.J., Fennelly J.A., Collins A.V., Harlos K.,
 RT Jones E.Y., Stuart D.I., Davis S.J.;
 RL "Structure and dimerization of a soluble form of B7-1.";
 RL Immunity 12:51-60(2000).
 CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
 CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
 CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
 CC RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES
 CC AND DENDRITIC CELLS.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD80 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd80.htm".
 CC -----
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 CC -----
 DR EMBL; M27533; AAA36045.1; -;
 DR EMBL; M83077; AAA58390.1; -;
 DR EMBL; M83072; AAA58390.1; JOINED.
 DR EMBL; M83073; AAA58390.1; JOINED.
 DR EMBL; M83074; AAA58390.1; JOINED.
 DR PIR; A45803; A45803.
 DR PIR; A45803; A45803.
 DR PDB; 1DR9; 10-JAN-01.
 DR Genew; HGNC:1700; CD80.
 DR MIM; 112203; -;
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003066; IG_MHC.
 DR InterPro; IPR003600; IG_Like.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00410; IG_Like; 1.
 DR Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor; 3D-structure.
 FT SIGNAL 1 34
 FT CHAIN 35 288
 FT DOMAIN 35 242
 FT TRANSMEM 243 263
 FT DOMAIN 264 288
 FT DOMAIN 43 123
 FT DOMAIN 155 223
 FT DISULFID 50 116
 FT DISULFID 162 216
 FT CARBOHYD 89 89
 FT CARBOHYD 98 98
 FT CARBOHYD 186 186
 FT CARBOHYD 207 207
 FT CARBOHYD 211 211
 FT CARBOHYD 226 226
 FT CARBOHYD 232 232
 FT SEQUENCE 288 AA; 33048 MW; BA453EE34528B1F4 CRC64;
 Query Match 10.1%; Score 161.5; DB 1; Length 288;
 Best Local Similarity 24.1%; Pred. No. 8e-06;
 Matches 57; Conservative 51; Mismatches 100; Indels 29; Gaps 11;
 QY 36 AYLPCPTKQAQNTLSLSLSELY---VFWQDQOKLVLYEHLVGTETKLDVSN--AKYLGRTSFD- 89
 DB 46 ATLSC---GHNVSVEELAQTRIVYQKEKMWL-----TMSGDMNIWPEYKNTIFDI 95

QY 90 RNNWTLRLHNVOIKDMSYDCFIQKXPPTGSIILQOTLTE--LSVIANFSEPEIKLAQNV 147
 DB 96 TNNLSIVILALRPSDEGYECVILKYEK--DAKREHLAEVTLVKADFTPTPSISDFEIP 153
 QY 148 TNSGNLNLTCTSKQHPKPKQMYFLITNSTNEYGDNMQISQDNVTELFSSINLSLSFPD 207
 DB 154 TSNIR-RIICSTSGGFPPEHLWS--LENGEELNAINTTVSQDPTETELYAVSSKLDNFNM-- 208
 QY 208 GVHMTVVCVLTESEMKISSKPLNFTQEPFSPQTYWKEITASVTVALLLVLLLIIVC 264
 DB 209 -TTNHFMCILKYHLRVNQ--TFNWNNTTKQHPDNPDLPLSWAITLISVNGIFVIC 261
 RESULT 9
 A33 HUMAN
 ID A33 HUMAN STANDARD; PRT; 319 AA.
 AC Q99795;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cell surface A33 antigen precursor (Glycoprotein A33).
 GN GPA33.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Colon carcinoma.
 RX MEDLINE=97165045; PubMed=9012807;
 RA Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
 RA Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
 RA Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
 RA Burgess A.W.;
 RT "The human A33 antigen is a transmembrane glycoprotein and a novel
 RT member of the immunoglobulin superfamily.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
 RN [2]
 RP POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=97396159; PubMed=9245713;
 RA Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
 RA Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
 RA Simpson R.J.;
 RT "Characterization of posttranslational modifications of human A33
 RT antigen, a novel palmitoylated surface glycoprotein of human
 RT gastrointestinal epithelium.";
 RL Biochem. Biophys. Res. Commun. 236:682-686(1997).
 CC -!- FUNCTION: MAY PLAY A ROLE IN CELL-CELL RECOGNITION AND SIGNALING.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN NORMAL GASTROINTESTINAL
 CC EPITHELIUM AND IN 95% OF COLON CANCERS.
 CC -!- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 K OF N-LINKED
 CC CARBOHYDRATE.
 CC -!- PTM: PALMITOYLATED.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -----
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 CC -----
 DR EMBL; U79725; AAC50957.1; -;
 DR Genew; HGNC:4445; GPA33.
 DR MIM; 602171; -;
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003600; IG_Like.
 DR InterPro; IPR003596; IG_v.

```

DR Pfam; PF00047; ig; 2.
DR SMART; SM00410; IG like; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
KW Transmembrane; Signal; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 319
FT DOMAIN 22 319
FT TRANSNEM 236 256
FT DOMAIN 257 319
FT DOMAIN 36 124
FT DOMAIN 139 229
FT DOMAIN 258 261
FT DISULFID 43 117
FT DISULFID 146 222
FT DISULFID 162 211
FT CARBOHYD 112 210
FT CARBOHYD 200 202
FT CARBOHYD 223 223
SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AAF45C2408E CRC64;

Query Match 9.1%; Score 146; DB 1; Length 319;
Best Local Similarity 24.5%; Pred. No. 0.00016;
Matches 79; Conservative 47; Mismatches 109; Indels 88; Gaps 19;

Qy 15 VTLLISDAVSVEV-----QAYFNGTAYLPCPTKAQN-----ISLSLWFW 57
Db 17 VTV-----DAISVETQDVLRSQGSVTLCTVHTSTSSREGLIQWDKLLLTHTERVW 72
Qy 58 QDOQKVLVHYLGTKEKLDVSNVAKYLGRTSFDNR-----NWLRLHNVQIKDMGSDYCFIQ 113
Db 73 PFSNK-----NYHGE-----LYKNRVSISSNNAEQSDASITIDQLTMDANGTYEC--- 117
Qy 114 KPPTGSIILQOVL-----TELSVIANFSEPEIKL-AQNVTGNSGINTCTSKOHPK 165
Db 118 -----SVSLMSDLGNTKSRVLLVLVPPSKPECEIGETIIIGN-IQLTCQSKGSPT 170
Qy 166 PK---KNYFLTNSVNEVDNQISQDNVTFLPSISNSLSFDPGVNHTVVCVLETES 222
Db 171 PQYSWKRY-----NINLQEQPLAQPASQGVSLKNISTDTS-----GYV---IC---TSS 214
Qy 223 MKISSKPLNFTQEPFSPQ---TYWKEITASVTVALLLVLLIIVCHKNPQSPRPNTAS 279
Db 215 NESGTOFCNITVAVSPSMNVALVGVAVGVAALIIIGIIVCCCR-----GRDNTED 270
Qy 280 KLERDNRADRETI-----NLKEL 297
Db 271 K--DARPNNREAYEPPPEQLREL 291

RESULT 10
SLAM_MOUSE STANDARD; PRT; 343 AA.
AC Q9QUH4; Q9QUX2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Signaling lymphocytic activation molecule precursor.
GN SLAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
RX MEDLINE=20040375; PubMed=10570270;
RA Castro A.G., Hauser T.M., Cocks B.G., Abrams J., Zurawski S.,
RA Churakova T., Zonin F., Robinson D., Tangye S.G., Aversa G.,
RA Nichols K.E., de Vries J.E., Lanier L.L., O'Garra A.;
RT "Molecular and functional characterization of mouse signaling
RT lymphocytic activation molecule (SLAM): differential expression and
RT responsiveness in Th1 and Th2 cells.";
J. Immunol. 163:5860-5870(1999).
[2]
SEQUENCE FROM N.A. (LONG ISOFORM).
Wang N., Wu C., Sayos J., Terhorst C.;
"Genomic organization of murine SLAM.";
Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: HIGH-AFFINITY SELF-LIGAND CONSIDERED TO BE IMPORTANT IN
CC BIDIRECTIONAL T <-> B-CELL STIMULATION. SLAM-INDUCED SIGNAL-
CC TRANSDUCTION EVENTS IN T LYMPHOCYTES ARE DIFFERENT FROM THOSE IN B
CC CELLS. TWO MODES OF SLAM SIGNALING ARE LIKELY TO EXIST: ONE IN
CC WHICH THE INHIBITOR SH2D1A ACTS AS A NEGATIVE REGULATOR AND
CC ANOTHER IN WHICH PROTEIN-TYROSINE PHOSPHATASE 2C (PTPN11)-
CC DEPENDENT SIGNAL TRANSDUCTION OPERATES.
CC -!- SUBUNIT: ITS CYTOPLASMIC DOMAIN INTERACTS WITH SH2 DOMAIN PROTEIN
CC 1A (SH2D1A) THROUGH PART OF ITS SH2 DOMAIN, AND UPON TYROSINE
CC PHOSPHORYLATION WITH PTPN11, BUT NOT WITH SHP-1.
CC -!- SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN; PRESENT ON THE
CC SURFACE OF B AND T CELLS.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- PTM: PHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
EMBL; AF149791; AAF22231.1; -
EMBL; AF149792; AAF22232.1; -
EMBL; AF164523; AAF13818.1; -
EMBL; AF164519; AAF13818.1; JOINED.
EMBL; AF164520; AAF13818.1; JOINED.
EMBL; AF164521; AAF13818.1; JOINED.
EMBL; AF164522; AAF13818.1; JOINED.
EMBL; AF160390; AAF14535.1; -
MGD; MGI:131314; Slam.
Receptor; Signal; Transmembrane; T-cell; Glycoprotein; Repeat;
Immunoglobulin domain; Phosphorylation; Alternative splicing.
FT SIGNAL 1 24
FT CHAIN 25 343
FT SIGNALING LYMPHOCYTIC ACTIVATION
FT MOLECULE.
FT DOMAIN 25 242
FT EXTRACELLULAR (POTENTIAL).
FT TRANSNEM 243 265
FT DOMAIN 266 343
FT DOMAIN ? 153
FT DOMAIN 154 239
FT DISULFID 161 232
FT DISULFID 167 212
FT SITE 286 291
FT SITE 313 318
FT SITE 333 338
FT CARBOHYD 54 54
FT CARBOHYD 58 58
FT CARBOHYD 103 103
FT CARBOHYD 126 126
FT CARBOHYD 151 151
FT CARBOHYD 158 158
FT CARBOHYD 192 192
FT CARBOHYD 211 211
FT CARBOHYD 226 226
FT VARSPLIC 296 343
SEQUENCE 343 AA; 38094 MW; 7980470157E834C4 CRC64;

Query Match 8.1%; Score 129.5; DB 1; Length 343;
Best Local Similarity 20.9%; Pred. No. 0.0036;

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Matches 75; Conservative 59; Mismatches 145; Indels 79; Gaps 14;
QY 1 MDPRCTMGLAILFVTVLLISDAVSQVETQAYFNGTAYLPCP----- 41
Db 1 MDPKGSLSWRLLFLSLAF-----ELSYGTGGVMDPCVILOKLQODTWLPLTNEHQ 52
QY 42 FTKAQNLSLSLVF-----WDOQKVLVYHYLGTETKLDLSVNAKYLGRTSFDRNNWTLR 96
Db 53 INKSNKSVRIIVTMATSPGSKNKKIVSPDLKSGYP-DHLEDGY----HFQSKNLSLK 107
QY 97 LHNVIQKMGSDYCFCKPPTGSIILQOITLTVLSVIANFSPEIKL-----AQNVTGNSG 152
Db 108 IIGNRSESGWYLSVEE-----NVSVOQCKQLKYEQVSPPEIKVINKTQENEGTCS 162
QY 153 INLCTSKQGHKPKMYFLITNSTNEYGDNMQISQDNVTFLFSINSLSLSPDGVYWHM 212
Db 163 LLLACTVKKGDH-----VTYWSDEAGTHLLSRNRSHLLH--TLSNQHQDSIYNC 212
QY 213 TVVCVLETFESMKISSKPLNFTQEPFSPOTYWKET---ASVTVALLLVLLIIVCHK--K 267
Db 213 TASNPVSIERTNLSQACKQESSSESSPMQVITLVLGVIIIFILVFTAILIMKKRQK 272
QY 268 PNQSRP-----SNTASKLERSDNADRE---TNLKLSPQIASA-KPN 307
Db 273 SNHCQPVVEKSLTIYAQVKSGPOEKKLHDALTDQDCTTIYVAATEPAPESQVEEN 330

RESULT 11
BUTY_HUMAN
ID BUTY_HUMAN STANDARD; PRT; 526 AA.
AC Q13410;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Butyrophilin precursor (BT).
GN BTN1AL OR BTN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RX MEDLINE=96201696; PubMed=8611614;
RA Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.;
RT "Cloning and sequence analysis of human butyrophilin reveals a
RT potential receptor function.";
RL Biochim. Biophys. Acta 1306:1-4(1996).
CC -!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC MEMBRANE (BY SIMILARITY).
CC -!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -----
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CC -----
CC EMBL: U39576; AAC50489.1; -.
CC Genes: HGNC:1135; BTN1AL.
CC MIM: 601610; -.
CC InterPro: IPR001870; Gamma_carboxylase.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
```

```
DR InterPro: IPR003878; SPRY domain.
DR InterPro: IPR003877; SPRY_receptor.
DR Pfam: PF00047; IS; 1.
DR Pfam: PF00822; SPRY; 1.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00449; SPRY; 1.
KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 26
FT CHAIN 27 526
FT DOMAIN 27 526 BUTYROPHILIN.
FT TRANSMEM 243 269 POTENTIAL.
FT TRANSMEM 270 526 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 526 AA; 59004 MW; E9EAC0CF8DAF94D5 CRC64;

Query Match 8.1%; Score 129.5; DB 1; Length 526;
Best Local Similarity 21.1%; Pred. No. 0.0063;
Matches 70; Conservative 59; Mismatches 142; Indels 61; Gaps 14;
QY 3 PRCTMGAILIFVTVLLISDAVSQVET-----QAYFNGTAYLPCPTKAQNLSLSLVV 55
Db 10 PRCLTLIILQLPKL----DSAPFDVIGPPEPILAVGDEDALEPCRL--SPNASAEHLLEL 63
QY 56 FW-QDOQKVLVYHYLGTETKLDLSVNAKYLGRTS-----FDRNNWTLRLHNVQIKONGSYD 109
Db 64 RWFRKKVSPAVLVHRDGRGQEAQEMPEYGRATLVQDGIAGRVLRIGRVVSDDEY 123
QY 110 CFIOKPPPTGSIILQOITLTVLSVIANFSPEIKLAQNVTGNSGINLTCTSKQGHKPKKM 169
Db 124 CFFRE---DGS---YEEALVHLKVAALGSDPHISM--QVQENGEICLECTSVGHYPQVQ 176
QY 170 YFIITNSTNEYGDNMQISQDNVTFLFSINSLSLSPDGVYWHMTVCVLETSKMKISSKP 229
Db 177 W--RTSGEKFPSTSESRNPDEGLEPTVAAS-----VIIRDSTKMWSCYI 220
QY 230 LNF-----TQFSPSPOTYWKET---ASVTVALLLVLLI-----VCHKKNQPS 272
Db 221 QNLLQLQEKVKVEISIPASSLPRLTPWIVAVAVILMVILGLTIGSIFFTWLYNERPRR 280
QY 273 RPSNTASKLERSDNADRETINLKE--LEFQIA 302
Db 281 NEFSSKRLLEELKKWKATLHAVDVTLDPDTA 312

RESULT 12
PVR2_HUMAN
ID PVR2_HUMAN STANDARD; PRT; 538 AA.
AC Q92692; O75455; Q96J29.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Herpes virus entry
DE mediator B) (HvB) (Nectin 2) (CD112 antigen).
GN PVR2L2 OR PRR2 OR HVBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=95347610; PubMed=7622062;
RA Eberle F., Dubreuil P., Mattei M.-G., Devillard E., Lopez M.;
RT "The human PRR2 gene, related to the human poliovirus receptor gene
RT (PVR), is the true homolog of the murine MPH gene.";
RL Gene 159:267-272(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=98321161; PubMed=9657005;
RA Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.;
RA Whitbeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G.;
RT "A cell surface protein with herpesvirus entry activity (HvB) confers
RT susceptibility to infection by mutants of herpes simplex virus type
```


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 CC -----
 CC EMBL; M88282; AAA36662.1; -;
 CC PIR; A46462; A46462;
 CC InterPro; IPR003599; IG_MHC.
 CC InterPro; IPR003006; IG_MHC.
 CC Pfam; PF00047; IG; 3.
 CC SMART; SM00409; IG; 1.
 CC Immunoglobulin domain; Glycoprotein; Transmembrane; Repeat; Signal.
 KW
 FT SIGNAL 1 21
 FT CHAIN 22 569
 FT DOMAIN 22 501
 FT TRANSMEM 502 525
 FT DOMAIN 526 569
 FT DOMAIN 534 486
 FT DOMAIN 538 547
 FT DOMAIN 38 125
 FT DOMAIN 156 238
 FT DOMAIN 267 346
 FT DISULFID 45 118
 FT DISULFID 163 231
 FT DISULFID 274 339
 FT CARBOHYD 42 42
 FT CARBOHYD 97 97
 FT CARBOHYD 107 107
 FT CARBOHYD 148 148
 FT CARBOHYD 156 156
 FT CARBOHYD 166 166
 FT CARBOHYD 184 184
 FT CARBOHYD 199 199
 FT CARBOHYD 261 261
 FT CARBOHYD 262 262
 FT CARBOHYD 284 284
 FT CARBOHYD 334 334
 FT CARBOHYD 352 352
 FT CARBOHYD 419 419
 FT CARBOHYD 481 481
 SQ SEQUENCE 569 AA; 63887 MW; DF2F3BEE356F3BF2 CRC64;
 Query Match 8.1%; Score 129.5; DB 1; Length 569;
 Best Local Similarity 24.4%; Pred. No. 0.007;
 Matches 77; Conservative 40; Mismatches 117; Indels 81; Gaps 15;
 QY 18 LIISDAYSVE-----TQAYENGTAIYPCPPTKQAQISLSLVVFWQ-----DQOKLVL 65
 DB 134 LIIOHTVADWNSHTIEINQTLIPCFQNSSSKIS-SEFYAWSVDNGTQETLIS 192
 QY 66 YEHVLGTGKLDVSNYAKLGRSFDNRNWLRLHNVQIKDMG-SYDCFIOKKPPTGSIIQL 124
 DB 193 QNHLSNSTLLKDRVK-LG-----TDYRLHLSVPQIFDDGRKFSCHIRVGP-----N 238
 QY 125 QTLTSLVIANFSEPEIKLAQVNGSGINL-----TCTSKQGHKPKKMYFLINTNSTNE 179
 DB 239 KILRSSTTVKFAKPEIPVI--VENNSTDLVERPFTCLKNVPPKANITWIDGSFLHD 296
 QY 180 YGDNMQIS-----QDNVTELSFI-----SNSLSLSPFDGWHMTVVCVLETESWKISK 229
 DB 297 EKEGIITNEERKKGDFLEKSVLTVHNSKPAQSONLTIWCWALSPVGNKVNWNISSE 356
 QY 229 PLNF-----TOEP-----SPQYMKELTASVTALLVLMLLIIV 263
 DB 357 KITFLLGSEISSTDPPLSVSTESTLDTQSPASSVSPARY--PATSSVT-----LVDV 406
 QY 264 CHKKNQPSRPSNTA 278
 DB 407 SALRENTTPQPSNSG 421

RESULT 14
 ID BUTY_BOVIN STANDARD; PRT; 526 AA.
 AC P18832; O18955; O18959;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Butyrophilin precursor (BT).
 GN BTN1A1 OR BTN.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
 RX MEDLINE=90354441; PubMed=2387867;
 RA Jack L.J.W., Mather I.H.;
 RT "Cloning and analysis of cDNA encoding bovine butyrophilin, an apical
 RT glycoprotein expressed in mammary tissue and secreted in association
 RT with the milk-fat globule membrane during lactation.";
 RL J. Biol. Chem. 265:14481-14486(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Holstein-Friesian;
 RA Davey H.W., Ogg S.L., Husaini Y., Snell R.G., Korobko I.V.,
 RA Mather I.H., Wilkins R.J.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Seyfert H., Luethen F.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=95293916; PubMed=7775382;
 RA Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.;
 RT Site-specific glycosylation of bovine butyrophilin.";
 RL J. Biochem. 117:147-157(1995).
 CC -!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
 CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
 CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
 CC (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
 CC ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
 CC SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -----
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 CC EMBL; M35551; AAB39766.1; -;
 CC EMBL; AF005497; AAB62889.1; -;
 CC EMBL; Z93323; CAB07533.1; -;
 CC PIR; A37821; A37821.
 CC InterPro; IPR001870; Gamma_carboxylase.
 CC InterPro; IPR003006; IG_MHC.
 CC InterPro; IPR003596; IG_V.
 CC InterPro; IPR003878; SPRY domain.
 CC InterPro; IPR003877; SPRY_receptor.
 CC Pfam; PF00047; IG; 1.
 CC Pfam; PF00622; SPRY; 1.

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DR SMART; SM00406; IGV; 1.  
DR SMART; SM00449; SPR; 1.  
KW Transmembrane, Glycoprotein; Immunoglobulin domain; Signal.  
FT SIGNAL 1 26  
FT CHAIN 27 526 BUTYROPHILIN.  
FT DOMAIN 27 242 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 243 269 POTENTIAL.  
FT DOMAIN 270 526 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).  
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (HYBRID).  
FT CONFLICT 35 35 Q -> P (IN REF. 3).  
FT CONFLICT 230 230 E -> D (IN REF. 1).  
SQ SEQUENCE 526 AA; 59276 MW; A14126802BD19284 CRC64;  
  
Query Match 8.1%; Score 129; DB 1; Length 526;  
Best Local Similarity 21.7%; Pred. No. 0.0069;  
Matches 73; Conservative 60; Mismatches 139; Indels 64; Gaps 15;  
  
QY 3 PRCTMGLAIIIFVTLIS-----DAVSVEIQ--AYFNGTAYLPCPTKAQNISLSSELV 54  
DB 5 PNSCIACGLDIFILQLPKLSAPFDVIGQEPILAVGSDAELPCRL--SPNVSAGME 62  
  
QY 55 VFM-QDOQKLVLYEHYLGTEKLDVSNAYKLGRTS-----FDRNNWTLRLHNVQIKDMGSY 108  
DB 63 LRMPREKVSFPAFVSREGQEGEGEMAEYGRVSLVEDHIAEGSVAVRIQEVKASDDGEY 122  
  
QY 109 DCFIQKPPGTSIILOOTLTLSLVIANFSEPEIKLAQNTVGNISGLNLTCTSKQGHKPKK 168  
DB 123 RCFFRQDN-----YEAAVHLVKVAALGSDPHISMVKVQESGE--TOLCTSVGVYPPQ- 174  
  
QY 169 MYFLITNSTNEYGDNNQISQDNVTELSFISNSLSLSPPD--GVYHMTVVCVLETESMKIS 226  
DB 175 -----VQWRTHRGEFFPSMSERN--PDEGLFTVRAVSIIRDSSMKV 216  
  
QY 227 S-----KPLNFTQ-----EFPSPQTYKKEITA-SVTVALLLVMLLII-----VCHKXP 268  
DB 217 SCCIRNLLGQKEVEVSIPASFPRLTPMVAVALVVLVGLLTIGSIFFTWRLYKERS 276  
  
QY 269 NQPSRPNTASKLRSDNADRETINLKE--LEPQIA 302  
DB 277 RQRNRFPSKELLELKWKRALHADVTLDPDTA 312  
  
RESULT 15  
ID JAM2 HUMAN STANDARD; PRT; 298 AA.  
AC P57087;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Junctional adhesion molecule 2 precursor (Vascular endothelial  
DE junction-associated molecule) (VE-JAM).  
GN JAM2 OR VEJAM OR C21ORF43.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Vascular endothelial cells;  
RX MEDLINE=20317114; PubMed=10779521;  
RA Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;  
RT "Vascular endothelial junction-associated molecule, a novel member of  
RT the immunoglobulin superfamily, is localized to intercellular  
RT boundaries of endothelial cells.";  
RL J. Biol. Chem. 275:19139-19145(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=20507930; PubMed=10945976;  
RA Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjerkce R.J.,  
RA Vanderslice P., Morris A.P., Brock T.A.;  
RT "A novel protein with homology to the junctional adhesion molecule:
```

Qy 268 ----PNQSRPONTASKLERDSNAD 288
 : ||: || |
Db 265 GYFSKETSFOKSNSSSKATTWSEND 289

Search completed: February 13, 2003, 11:31:41
Job time : 18.4671 secs

GenCore version 5.1.1.3

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OM protein - protein search, using sw model

Run on: February 13, 2003, 11:28:39 ; Search time 27.6066 Seconds
(without alignments)
2306.282 Million cell updates/sec

Title: US-09-425-516-23

Perfect score: 1599

Sequence: 1 MDPRCTMGGLAIFVTVLLI.....ETINLUKELEPOIASAKPNAE 309

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_virus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1579	98.7	309	11 Q91YV7	Q91YV7 mus musculus
2	1576	98.6	314	11 Q61238	Q61238 mus musculus
3	1567	98.0	356	11 Q64381	Q64381 mus musculus
4	1027	64.2	313	11 Q35531	Q35531 rattus norv
5	709.5	44.4	323	6 Q9BDW2	Q9BDW2 cercopithec
6	705.5	44.1	323	6 Q9BDW4	Q9BDW4 macaca mula
7	701.5	43.9	323	6 Q9BDW8	Q9BDW8 cercocebus
8	694	43.4	329	6 Q9TTF2	Q9TTF2 canis famil
9	689.5	43.1	323	6 Q9BDW9	Q9BDW9 macaca nome
10	662	41.4	325	6 Q02838	Q02838 sus scrofa
11	658	41.2	280	6 Q9TTF1	Q9TTF1 canis famil
12	652	40.8	149	11 Q62810	Q62810 rattus norv
13	650.5	40.7	275	6 Q9BDN9	Q9BDN9 papio anubi
14	640.5	40.1	329	6 Q9XSX6	Q9XSX6 felis silve
15	640.5	40.1	332	6 Q9GMZ7	Q9GMZ7 felis silve
16	640.5	40.1	332	6 Q95L16	Q95L16 felis silve

17	585	36.6	284	6 Q9GL33	Q9GL33 bos taurus
18	226.5	14.2	306	11 Q9R129	Q9R129 mus musculu
19	223	13.9	321	11 Q62624	Q62624 rattus norv
20	217	13.6	321	11 Q55202	Q55202 rattus norv
21	215	13.4	321	11 Q35187	Q35187 rattus norv
22	210	13.1	316	11 Q8VE98	Q8VE98 mus musculu
23	206	12.9	290	11 Q62680	Q62680 rattus norv
24	180.5	11.3	304	6 Q9TQX1	Q9TQX1 canis famil
25	176	11.0	296	6 Q46405	Q46405 bos taurus
26	176	11.0	316	4 Q9BXR1	Q9BXR1 homo sapien
27	175.5	11.0	292	6 Q9CMZ8	Q9CMZ8 felis silve
28	175.5	11.0	292	6 Q02758	Q02758 felis silve
29	170.5	10.7	297	6 Q9BE99	Q9BE99 sus scrofa
30	170.5	10.7	567	4 Q96KV6	Q96KV6 homo sapien
31	168	10.5	296	6 Q8WMZ2	Q8WMZ2 sus scrofa
32	164.5	10.3	235	6 Q9N0T0	Q9N0T0 canis famil
33	164.5	10.3	235	6 Q9TOS8	Q9TOS8 canis famil
34	164.5	10.3	288	6 Q9TT70	Q9TT70 sus scrofa
35	163	10.2	334	4 Q96AV7	Q96AV7 homo sapien
36	163	10.2	527	4 Q00475	Q00475 homo sapien
37	162.5	10.2	288	6 Q77684	Q77684 macaca mula
38	160.5	10.0	288	6 Q28499	Q28499 macaca mula
39	156	9.8	229	6 Q9TT71	Q9TT71 sus scrofa
40	156	9.8	230	6 Q9N2I3	Q9N2I3 sus scrofa
41	156	9.8	414	4 Q9UM44	Q9UM44 homo sapien
42	148.5	9.3	220	4 Q9NQ06	Q9NQ06 homo sapien
43	148.5	9.3	226	13 Q42404	Q42404 gallus gall
44	144.5	9.0	288	6 Q9BDN6	Q9BDN6 cercocebus
45	144.5	9.0	289	6 Q28347	Q28347 cercocebus

ALIGNMENTS

RESULT 1

Q91YV7 PRELIMINARY; PRT; 309 AA.
 AC Q91YV7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE CD86 antigen.
 GN CD86.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013807; AAH13807.1; -.
 DR MGD; MGI:101773; CG86.
 SQ SEQUENCE 309 AA; 34714 MW; 61593C49EFCB0CE5 CRC64;

Query Match 98.7%; Score 1579; DB 11; Length 309;
 Best Local Similarity 99.0%; Pred No. 4.7e-129;
 Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDPRCTMGGLAIFVTVLLISDAVSVEVETQAYFNGTAYLPCPFTKAQNISLSLVFWQDQ 60
 |||||
 Db 1 MDPRCTMGGLAIFVTVLLISDAVSVEVETQAYFNGTAYLPCPFTKAQNISLSLVFWQDQ 60
 |||||
 QY 61 QKLVLYEHLCTEKLDSDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKPEPTGS 120
 |||||
 Db 61 QKLVLYEHLCTEKLDSDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKPEPTGS 120
 |||||
 QY 121 IILQOTLTSLVIANFSEPIKLAQNVTGNSGINTCTSKQGHPPKPKMYFLITNSTNEY 180
 |||||
 Db 121 IILQOTLTSLVIANFSEPIKLDQNVTCGNSGINTCTSKQGHPPKPKMYFLITNSTNEY 180
 |||||
 QY 181 GDNMOISDQNVTELFSSNSLSLSPFDGVVHMTVVVCLVETESMKISSKPLNFTQEPSPQ 240
 |||||

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Db 181 GDNMQISQDNVTLEFSISNSLSLSPDPGVHMTVVCULETESMKISSKPLNFTOEPPSAQ 240
Qy 241 TYWKEITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQ 300
Db 241 TYWKEITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQ 300
Qy 301 IASAKPNAE 309
Db 301 IASAKPNAE 309

RESULT 2
ID Q61238 PRELIMINARY; PRT; 314 AA.
AC Q61238;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE B7-2 protein.
GN CD86 OR B7-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=96094437; PubMed=7499829;
RA Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;
RT "Differential expression of alternate mB7-2 transcripts.";
RL J. Immunol. 155:5490-5497(1995).
DR EMBL; U39456; AAC52335.1; JOINED.
DR EMBL; U39460; AAC52335.1; JOINED.
DR EMBL; U39461; AAC52335.1; JOINED.
DR EMBL; U39462; AAC52335.1; JOINED.
DR EMBL; U39463; AAC52335.1; JOINED.
DR EMBL; U39464; AAC52335.1; JOINED.
DR EMBL; U39465; AAC52335.1; JOINED.
DR MGD; MGI:101773; Cd86.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
SQ SEQUENCE 314 AA; 35177 MW; 3D2683F36CAEDF4 CRC64;

Query Match 98.6%; Score 1576; DB 11; Length 314;
Best Local Similarity 100.0%; Pred. No. 8.7e-129;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CTMGLAILIFVTLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLSELVFVWQDQKLV 64
Db 10 CTMGLAILIFVTLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLSELVFVWQDQKLV 69
Qy 65 LYHYLGTGKLDVSNAYKLGRTSFDNRNWTLRHNVQIKDMGSYDCFIQKKPPTGSIILQ 124
Db 70 LYHYLGTGKLDVSNAYKLGRTSFDNRNWTLRHNVQIKDMGSYDCFIQKKPPTGSIILQ 129
Qy 125 QTLTSLVIANFSEPIKLAQNVGTGSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNM 184
Db 130 QTLTSLVIANFSEPIKLAQNVGTGSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNM 189
Qy 185 QISQDNVTLEFSISNSLSLSPDPGVHMTVVCULETESMKISSKPLNFTOEPPSPQYWK 244
Db 190 QISQDNVTLEFSISNSLSLSPDPGVHMTVVCULETESMKISSKPLNFTOEPPSPQYWK 249
Qy 245 EITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQIASA 304
Db 250 EITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQIASA 309
Qy 305 KPNAE 309
Db 310 KPNAE 314
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RESULT 3
Q64381
ID Q64381 PRELIMINARY; PRT; 356 AA.
AC Q64381;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE B7-2.
GN CD86 OR B7-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=96094437; PubMed=7499829;
RA Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;
RT "Differential expression of alternate mB7-2 transcripts.";
RL J. Immunol. 155:5490-5497(1995).
DR EMBL; U39456; AAC52333.1; JOINED.
DR EMBL; U39457; AAC52333.1; JOINED.
DR EMBL; U39461; AAC52333.1; JOINED.
DR EMBL; U39462; AAC52333.1; JOINED.
DR EMBL; U39463; AAC52333.1; JOINED.
DR EMBL; U39464; AAC52333.1; JOINED.
DR EMBL; U39465; AAC52333.1; JOINED.
DR EMBL; U39466; AAC52333.1; JOINED.
DR EMBL; U39467; AAC52333.1; JOINED.
DR EMBL; U39468; AAC52333.1; JOINED.
DR EMBL; U39469; AAC52333.1; JOINED.
DR EMBL; U39470; AAC52333.1; JOINED.
DR EMBL; U39471; AAC52333.1; JOINED.
DR EMBL; U39472; AAC52333.1; JOINED.
DR EMBL; U39473; AAC52333.1; JOINED.
DR MGD; MGI:101773; Cd86.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
SQ SEQUENCE 356 AA; 39860 MW; 9EF13B74308F3514 CRC64;

Query Match 98.0%; Score 1567; DB 11; Length 356;
Best Local Similarity 100.0%; Pred. No. 6.2e-128;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TMGLAILIFVTLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLSELVFVWQDQKLV 65
Db 53 TMGLAILIFVTLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLSELVFVWQDQKLV 112
Qy 66 YEHYLGTEKLDVSNAYKLGRTSFDNRNWTLRHNVQIKDMGSYDCFIQKKPPTGSIILQ 125
Db 113 YEHYLGTEKLDVSNAYKLGRTSFDNRNWTLRHNVQIKDMGSYDCFIQKKPPTGSIILQ 172
Qy 126 TLTSLVIANFSEPIKLAQNVGTGSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNM 185
Db 173 TLTSLVIANFSEPIKLAQNVGTGSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNM 232
Qy 186 IQSDNVTELFISNSLSLSPDPGVHMTVVCULETESMKISSKPLNFTOEPPSPQYWK 245
Db 233 IQSDNVTELFISNSLSLSPDPGVHMTVVCULETESMKISSKPLNFTOEPPSPQYWK 292
Qy 246 ITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQIASAK 305
Db 293 ITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQIASAK 352
Qy 306 PNAE 309
Db 353 PNAE 356

RESULT 4
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O35531
ID O35531 PRELIMINARY; PRT; 313 AA.
AC
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Membrane glycoprotein precursor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN-WISTAR LEWIS; TISSUE-LYMPHOMA;
RX MEDLINE=97380318; PubMed=92371108;
RA Maeda K., Sato T., Azuma M., Yagita H., Okumura K.;
RT "Characterization of rat CD80 and CD86 by molecular cloning and mAb.";
RL Int. Immunol. 9:993-1000(1997).
DR EMBL; D50558; BAA23470.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 29 POTENTIAL.
FT CHAIN 30 313 CD28 AND CTLA4 LIGAND.
SQ SEQUENCE 313 AA; 35573 MW; 3106246B8901B5D5 CRC64;

Query Match 64.2%; Score 1027; DB 11; Length 313;
Best Local Similarity 68.6%; Pred. No. 4.1e-81;
Matches 210; Conservative 29; Mismatches 53; Indels 14; Gaps 5;

QY 5 CTMGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPTKAQNISLSLVFWQDOOKLV 64
DB 10 CTMGLILFSLVLAFLSDAVPVKQAYFNSTAYLPCPTKAQNISLSLVFWQDKKSV 69

QY 65 LYEHYLGTEKLDVNAKYLQRTSFRDNWTLRLHNVIQKMGSYDCFIQKKPTGSIILQ 124
DB 70 LYEHYLGAEKLDVNAKYLQRTSFRDNQALRLHNVIQKDTGLYDCFIQKKPTGSIILQ 129

QY 125 QTLTSLVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNM 184
DB 130 QWETLSVIANFSEPEIEEQNETRNTGINTCTSSKQGYPKPTKMYFLITNSTNEYGDNM 189

QY 185 QISQDNVTELSISLSLSPDGVVHMTVVCVLETESMKISSKPLNFTQEPSPQ---T 241
DB 190 QISQDNVTKLFSVLSLSPDGVVHMTVVCVLETESMNISSKPHNMV--FSQPQFORK 247

QY 242 YWKEITASVTVALLLVIV-----CHKKNOPSPSNTASKLERDSNADRETINLK 295
DB 248 TWIQIAG--PSSLICCLFLIVVYKAVKCLKMKNQPGRPSPKTCESKQDSGVD-ESINLE 304

QY 296 ELEPQI 301
DB 305 EVERPOL 310

RESULT 5
Q9BDM2 PRELIMINARY; PRT; 323 AA.
ID Q9BDM2
AC Q9BDM2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CD86 protein.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
SEQUENCE FROM N.A.
RC MEDLINE=21383618; PubMed=11491535;
RX Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344861; AAK37543.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 323 AA; 37019 MW; D211E103DB1A7D7A CRC64;

Query Match 44.1%; Score 705.5; DB 6; Length 323;
Best Local Similarity 51.2%; Pred. No. 3.6e-53;
```

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RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344861; AAK37543.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
SQ SEQUENCE 323 AA; 37045 MW; 3E43152A8FD17267 CRC64;

Query Match 44.4%; Score 709.5; DB 6; Length 323;
Best Local Similarity 51.2%; Pred. No. 1.6e-53;
Matches 154; Conservative 41; Mismatches 93; Indels 13; Gaps 5;

QY 7 MGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPTKAQNISLSLVFWQDOOKLVLY 66
DB 1 MGLINILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSONRSLSELVVPWQENLVLN 60

QY 67 EHYLGTEKLDVNAKYLQRTSFRDNWTLRLHNVIQKMGSYDCFIQKKPTGSIILQOT 126
DB 61 EYVLGOEKFDVSHSKYMGRTSFDPSWTLLHLNLIQKDKGLYQCIIHHRKPTGMIRIHO 120

QY 127 LTSLVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKKMYFLI--TNSTNEYGDNM 184
DB 121 NSELVIANFSEPEIVPISNITENWYINLTCSIHGYPEPEKMSVLLRTKNSTIYDGVN 180

QY 185 QISQDNVTELSISLSLSPDGVVHMTVVCVLETESMKISSKPLNFTQEPSPQ---QT 241
DB 181 QKSQDNVTELYDSVLSLSPDVTNMTIFCVLETDTKTLQLLSSPFSIELEDPPQPPDHI 240

QY 242 YWKEITASVTVALLLVIV--LLIIVCHKXP---NOPSRSNTASKLERDSNADRETINLK 295
DB 241 PW--ITAVLPTVILCWAFCLILWKCKKKKQPNYSYKRGNTNWEREESQTKKEKINVP 298

QY 296 E 296
DB 299 E 299

RESULT 6
Q9BDM4 PRELIMINARY; PRT; 323 AA.
ID Q9BDM4
AC Q9BDM4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CD86 protein precursor.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
SEQUENCE FROM N.A.
RC MEDLINE=21383618; PubMed=11491535;
RX Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344857; AAK37540.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 323 AA; 37019 MW; D211E103DB1A7D7A CRC64;

Query Match 44.1%; Score 705.5; DB 6; Length 323;
Best Local Similarity 51.2%; Pred. No. 3.6e-53;
```

Matches 154; Conservative 41; Mismatches 93; Indels 13; Gaps 5;

QY 7 MGLAIIIFVTVLLISDAVSVEVETQAYFNGTAYLPCPFTKAQNISLSLVVFWQDQOKLVLY 66
 Db 1 MGLSILFVMAFLUSGAAPLKIQAYFNETADLPQCFANSQNRSLSELVFWQENLVN 60
 QY 67 EHYLGTCKLDSVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGSILOOT 126
 Db 61 EYVLGKRFDSVHSHKYGWRTSFPDSWTLRLHNLOIKDKGLYQCIHHKRPCTGMIRHQM 120
 QY 127 LTELAVIANFSEPEIKLAQNVNCGINLTCTSKOGHPKPKMYFLI--TNSTNEYGDMN 184
 Db 61 EYVLGKRFDSVHSHKYGWRTSFPDSWTLRLHNLOIKDKGLYQCIHHKRPCTGMIRHQM 120
 QY 121 NSELVLANFQSQEIPVPSINITENMYINLTCSIHGYPEPEKMSVLLRTKNPTIEYDGYM 180
 QY 127 LTELAVIANFSEPEIKLAQNVNCGINLTCTSKOGHPKPKMYFLI--TNSTNEYGDMN 184
 Db 121 NSELVLANFQSQEIPVPSINITENMYINLTCSIHGYPEPEKMSVLLRTKNPTIEYDGYM 180
 QY 185 QISQDNVTLEISNSLSLSPGQVHMVTVCVLETESMKISSKPLNFTQEPFSP---QT 241
 Db 181 OKSQDNVTLEISNSLSLSPGQVHMVTVCVLETESMKISSKPLNFTQEPFSP---QT 241
 QY 242 YKKEITASVTVALLLVM--LLIIVCHKKPNQPSRP----SNTASKLERDSNADRETINLK 295
 Db 241 PW--ITAVLPTVIICVMAFLCLILWKWKKKQPRNSYKCGTNTMERESQTKKREKINVP 298
 QY 296 E 296
 Db 299 E 299

RESULT 7
 Q9BDB8 PRELIMINARY; PRT; 323 AA.

ID Q9BDB8
 AC Q9BDB8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CD86 protein precursor.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Cercopithecinae; Cercopithecidae;
 OC NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Boetik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 Fas/Fas-ligand and co-stimulatory molecules."
 RL Immunogenetics 53:315-328(2001).
 DR EMBL; AF344840; AAK37536.1; -.
 DR InterPro; IPR003599; IG v.
 DR SMART; SM00409; IG v.
 DR SMART; SM00406; IGv; 1.
 KW Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 323
 FT VARIANT 26 26
 FT VARIANT 97 97
 FT VARIANT 138 138
 FT VARIANT 147 147
 FT VARIANT 166 166
 FT VARIANT 172 172
 FT VARIANT 206 206
 FT VARIANT 260 260
 FT VARIANT 284 284
 FT VARIANT 319 319
 FT VARIANT 322 322
 SQ SEQUENCE 323 AA; 37010 MW; 45B217C606A79B75 CRC64;

Query Match 43.98; Score 701.5; DB 6; Length 323;
 Best Local Similarity 50.8%; Pred. No. 8e-53; Indels 13; Gaps 5;
 Matches 153; Conservative 42; Mismatches 93; Indels 13; Gaps 5;

QY 7 MGLAIIIFVTVLLISDAVSVEVETQAYFNGTAYLPCPFTKAQNISLSLVVFWQDQOKLVLY 66
 Db 1 MGLSILFVMAFLUSGAAPLKIQAYFNETADLPQCFANSQNRSLSELVFWQENLVN 60
 QY 67 EHYLGTCKLDSVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGSILOOT 126
 Db 61 EYVLGKRFDSVHSHKYGWRTSFPDSWTLRLHNLOIKDKGLYQCIHHKRPCTGMIRHQM 120
 QY 127 LTELAVIANFSEPEIKLAQNVNCGINLTCTSKOGHPKPKMYFLI--TNSTNEYGDMN 184
 Db 61 EYVLGKRFDSVHSHKYGWRTSFPDSWTLRLHNLOIKDKGLYQCIHHKRPCTGMIRHQM 120
 QY 121 NSELVLANFQSQEIPVPSINITENMYINLTCSIHGYPEPEKMSVLLRTKNPTIEYDGYM 180
 QY 185 QISQDNVTLEISNSLSLSPGQVHMVTVCVLETESMKISSKPLNFTQEPFSP---QT 241
 Db 181 OKSQDNVTLEISNSLSLSPGQVHMVTVCVLETESMKISSKPLNFTQEPFSP---QT 241
 QY 242 YKKEITASVTVALLLVM--LLIIVCHKKPNQPSRP----SNTASKLERDSNADRETINLK 295
 Db 241 PW--ITAVLPTVIICVMAFLCLILWKWKKKQPRNSYKCGTNTMERESQTKKREKINVP 298
 QY 296 E 296
 Db 299 E 299

RESULT 8
 Q9TTT2 PRELIMINARY; PRT; 329 AA.

ID Q9TTT2
 AC Q9TTT2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE B7-2 protein.
 GN CD86.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20093996; PubMed=10630300;
 RA Yang S., Sim G.-K.;
 RT "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
 Molecules."
 RL Immunogenetics 50:349-353(1999).
 DR EMBL; AF106826; AAF17297.1; -.
 DR HSP; P33681; 1DR9.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 329 AA; 37774 MW; D98BB63437BF7B73 CRC64;

Query Match 43.4%; Score 694; DB 6; Length 329;
 Best Local Similarity 49.0%; Pred. No. 3.7e-52;
 Matches 154; Conservative 50; Mismatches 80; Indels 30; Gaps 11;

QY 4 RCTMGLAIIIFVTVLLISDAVSVEVETQAYFNGTAYLPCPFTKAQNISLSLVVFWQDQOKL 63
 Db 4 RCTMELNNILFVMTLLLYCAASMKSQAYFNKGTGELPCHFTNSQNSLDELVFWQDQOKL 63
 QY 64 VLYEHVLTGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGSIIL 123
 Db 64 VLYELVYRGKENQNVHRYKGTSTFDKDNWTLRLHNIQIKDKGLYQCFVHHKPKGLVPM 123
 QY 124 QQTLELSVIANFSEPEIKLAQNVNCGINLTCTSKOGHPKPKMYFLI--TNSTNEY 180
 Db 124 HOMNSDLVLANFQSQEIPVPSINITENMYINLTCSIHGYPEPEKMYFLVKTENSTKY 183
 QY 181 GDNWQISQDNVTLEISNSLSLSPGQVHMVTVCVLETESMKISSKPLNFTQEPFSP 239
 Db 184 DTVMKKSQNNVTLEISNSLSLSPGQVHMVTVCVLETESMKISSKPLNFTQEPFSP 242


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Qy 240 ---QTYWKEITASVTVALLLVLLIIVC-----HKKPNQSPSPN--TASKLER-D 284
Db 243 DGDHILW-----IALLLWM-LVILCGMVFFTLRKRRKKQPG-PSHECETNKVERKE 292
Qy 285 SNADRETINKLELE 298
Db 293 SEQTKERVRYHETE 306

RESULT 9
Q9BDM9 PRELIMINARY; PRT; 323 AA.
AC Q9BDM9;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CD86 protein precursor.
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Boetik P., Wayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344851; AAK37611.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 323 AA; 37079 MW; C6C8E2F125C647FD CRC64;
Query Match 43.1%; Score 689.5; DB 6; Length 323;
Best Local Similarity 50.5%; Pred. No. 8.8e-52;
Matches 152; Conservative 41; Mismatches 95; Indels 13; Gaps 5;
Qy 7 MGLAILFVTVLLISDAVSVEVETQAYFNGTAYLPCPFTKAQNISLSLVVFWODQOKLVLY 66
Db 1 MGLSNILFVWVLLSGLSAAKQAYFNETGELPCHFTNSQNLSDLVIFWODQONLVLY 60
Qy 67 EHYLGTBKLDSVNAKYLGRTSFDRNNTLRLHNQIKDMGSYDCFIQKKPPTGSIILQQT 126
Db 61 EYVLGKEKFDVSHKYMGRTRDPESWTILRLNLQIKDKGLYQCIHHKRPFGMRHQM 120
Qy 127 LTELVSIVANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKKMYFLIT--NSTWEYGDNM 184
Db 121 NSELVSIVANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKKMYFLIT--NSTWEYGDNM 180
Qy 185 QISQDNVTELFSSNSLSLSPDPGVVHMTVVCVLETESMK--ISSKPLNFTOFFPSPQTY 242
Db 181 KKSQNNITELVNVSVIRVPIPET-NVSVICVLQLEPSKTLFLSPCNIDAKPPVQPPV 239
Qy 243 WKEITASVTVALLLVLLIIVC-----HKKPNQSPSPN--TASKLER-D 284
Db 240 PDHI---LWTAALLV-TVVWCVGVSFVTLRKRKKQPGSPNEGETIKMNRKASEQTKN 295
Qy 294 LKELEPQIASAK 305
Db 296 RAEVHERSDDAQ 307

RESULT 10
Q9TTF1 PRELIMINARY; PRT; 280 AA.
AC Q9TTF1;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Truncated B7-2 protein.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20093996; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
RT Molecules.";
RL Immunogenetics 50:349-353(1999).
DR EMBL; AF106827; AAF17298.1; -.
DR HSSP; P33681; IDR9.
```

```
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE B7-2.
GN CD86.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97047772; PubMed=8892613;
RA Maher S.E., Karmann K., Min W., Hughes C.C., Pober J.S.,
RA Bothwell A.L.;
RT "Porcine endothelial CD86 is a major costimulator of xenogeneic human
RT T cells: cloning, sequencing, and functional expression in human
RT endothelial cells.";
RL J. Immunol. 157:3838-3844(1996).
DR EMBL; L76099; AAB61307.1; -.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
SQ SEQUENCE 325 AA; 36527 MW; 988BE08137B0597D CRC64;
Query Match 41.4%; Score 662; DB 6; Length 325;
Best Local Similarity 45.5%; Pred. No. 2.2e-49;
Matches 142; Conservative 57; Mismatches 95; Indels 18; Gaps 6;
Qy 7 MGLAILFVTVLLISDAVSVEVETQAYFNGTAYLPCPFTKAQNISLSLVVFWODQOKLVLY 66
Db 1 MGLSNILFVWVLLSGLSAAKQAYFNETGELPCHFTNSQNLSDLVIFWODQONLVLY 60
Qy 67 EHYLGTBKLDSVNAKYLGRTSFDRNNTLRLHNQIKDMGSYDCFIQKKPPTGSIILQQT 126
Db 61 EYLRQGEKPHNVSKYMGRTSFDQATWTLRLHNQIKDKGSYQCFIHHKGPGLVPIHQM 120
Qy 127 LTELVSIVANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKKMYFLIT--NSTWEYGDNM 184
Db 121 SDSLILANFSQPEINLTNTHTNSVINLTCSSTQGYPEFQRMVLLNTKNTSTTHDADM 180
Qy 185 QISQDNVTELFSSNSLSLSPDPGVVHMTVVCVLETESMK--ISSKPLNFTOFFPSPQTY 242
Db 181 KKSQNNITELVNVSVIRVPIPET-NVSVICVLQLEPSKTLFLSPCNIDAKPPVQPPV 239
Qy 243 WKEITASVTVALLLVLLIIVC-----HKKPNQSPSPN--TASKLER-D 284
Db 240 PDHI---LWTAALLV-TVVWCVGVSFVTLRKRKKQPGSPNEGETIKMNRKASEQTKN 295
Qy 294 LKELEPQIASAK 305
Db 296 RAEVHERSDDAQ 307

RESULT 11
Q9TTF1 PRELIMINARY; PRT; 280 AA.
AC Q9TTF1;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Truncated B7-2 protein.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20093996; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
RT Molecules.";
RL Immunogenetics 50:349-353(1999).
DR EMBL; AF106827; AAF17298.1; -.
DR HSSP; P33681; IDR9.
```

[illegible]

FT Domain /label= Transmembrane_domain
FT 266..309
XX /label= Cytoplasmic_domain
PN W09640915-A2.
XX
XX 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US09052.
XX
XX 07-JUN-1995; 95US-0479744.
XX
XX (DAND) DANA FARBER CANCER INST INC.
PA (REPK) REPLIGEN CORP.
XX
XX Freeman GJ, Gray GS, Nadler LM;
PI
XX WPI; 1997-07269/07.
DR N-PSDB; AAT49182.
XX
XX DNA encoding a B7-2 fusion protein - used to enhance or down
PT regulate B lymphocyte antigens
XX
XX Example 6; Page 102-103; 171pp; English.

DE Mouse B7-2 antigen.
XX
KW B7-2 antigen; mammalian tumour cell; T cell costimulation; CD28 ligand;
KW CTLA4 ligand; therapy; T-cell response; mouse.
XX
OS Mus sp.
XX
PN U85861310-A.
XX
PD 19-JAN-1999.
XX
XX 30-MAY-1995; 95US-0456104.
PF
XX 30-MAY-1995; 95US-0456104.
PR
XX 03-NOV-1993; 93US-0147773.
XX
PA (DAND) DANA FARBER CANCER INST INC.
XX
XX Freeman GJ, Gray GS, Nadler LM;
PI
XX WPI; 1999-130394/11.
DR N-PSDB; AAV55785.
XX
XX Tumour cell transfected to express B7-2 molecule - useful for tumour
PT therapy by stimulating T-cell response
XX
XX Disclosure; Column 31-34; 27pp; English.
PS
XX This sequence is the mouse B7-2 antigen, which can be used in the
CC method of the invention. The method is for transfecting an isolated
CC mammalian tumour cell with an exogenous nucleic acid molecule encoding a
CC mammalian B7-2 molecule, where the B7-2 molecule is expressed in the
CC tumour cell is capable of costimulating a T cell and is capable of
CC binding a CD28 or CTLA4 ligand. The method is useful for treating tumours
CC by stimulating a T-cell response against tumour cells in vivo.
XX
SQ Sequence 309 AA;

Query Match 100.0%; Score 1599; DB 18; Length 309;
Best Local Similarity 100.0%; Pred. No. 1e-127;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDPRTCTMGALILIFVTVLLISDAVSVEQAYFNGTAYILPCPFTKAQNISLSLWVWQDQ 60
DB 1 MDPRTCTMGALILIFVTVLLISDAVSVEQAYFNGTAYILPCPFTKAQNISLSLWVWQDQ 60
QY 61 QKLVLVEHYLGTETKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPTGS 120
DB 61 QKLVLVEHYLGTETKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPTGS 120
QY 121 IILQOTLTLSLVIANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKKMYFLITNSTNEY 180
DB 121 IILQOTLTLSLVIANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKKMYFLITNSTNEY 180
QY 181 GDNMOISQDNVTLEFSISLSLSPFDGVVHMTVVCVLETESMKISSKPLNFTQEPSPQ 240
DB 181 GDNMOISQDNVTLEFSISLSLSPFDGVVHMTVVCVLETESMKISSKPLNFTQEPSPQ 240
QY 241 TYWKEITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERSNADRETINLKELEPQ 300
DB 241 TYWKEITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERSNADRETINLKELEPQ 300
QY 301 IASAKPNAE 309
DB 301 IASAKPNAE 309

Query Match 100.0%; Score 1599; DB 20; Length 309;
Best Local Similarity 100.0%; Pred. No. 1e-127;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDPRTCTMGALILIFVTVLLISDAVSVEQAYFNGTAYILPCPFTKAQNISLSLWVWQDQ 60
DB 1 MDPRTCTMGALILIFVTVLLISDAVSVEQAYFNGTAYILPCPFTKAQNISLSLWVWQDQ 60
QY 61 QKLVLVEHYLGTETKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPTGS 120
DB 61 QKLVLVEHYLGTETKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPTGS 120
QY 121 IILQOTLTLSLVIANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKKMYFLITNSTNEY 180
DB 121 IILQOTLTLSLVIANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKKMYFLITNSTNEY 180
QY 181 GDNMOISQDNVTLEFSISLSLSPFDGVVHMTVVCVLETESMKISSKPLNFTQEPSPQ 240
DB 181 GDNMOISQDNVTLEFSISLSLSPFDGVVHMTVVCVLETESMKISSKPLNFTQEPSPQ 240
QY 241 TYWKEITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERSNADRETINLKELEPQ 300
DB 241 TYWKEITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERSNADRETINLKELEPQ 300
QY 301 IASAKPNAE 309
DB 301 IASAKPNAE 309

RESULT 2
AAW73639
ID AAW73639 standard; Protein; 309 AA.
XX
AC AAW73639;
XX
DT 23-MAR-1999 (first entry)
XX

RESULT 3
AAB37086
ID AAB37086 standard; Protein; 309 AA.
XX
AC AAB37086;
XX

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XX 28-MAR-2001 (first entry)
XX Mouse B lymphocyte antigen B7-2.
XX Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;
XX antigen; extracellular domain; CTLA4; immunoglobulin constant region;
XX immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage;
XX T cell-mediated immune response; transplantation; vaccination.
XX OS sp.
XX US6130316-A.
XX 10-OCT-2000.
XX 26-JUL-1994; 94US-0280757.
XX 26-JUL-1993; 93US-0101624.
XX 19-AUG-1993; 93US-0109393.
XX 03-NOV-1993; 93US-0147773.
XX (DAND ) DANA FARBER CANCER INST INC.
XX PA (REPK ) REPLIGEN CORP.
XX Freeman GJ, Nadler LM, Gray GS, Greenfield E;
XX WPI; 2000-655681/63.
XX N-PSDB; AAC84050.
XX Nucleic acids and fusion proteins of CTLA4/CD28 ligands, useful for
XX enhancing or suppressing T cell-mediated immune responses, especially
XX during tissue, skin or organ transplantation, or in graft-versus-host
XX disease -
XX Example 6; Fig 14; 83pp; English.
XX The invention relates to an isolated nucleic acid molecule encoding a
XX fusion protein comprising a first nucleotide sequence encoding a first
XX peptide, and a second nucleotide sequence encoding a second peptide.
XX The first nucleotide sequence hybridizes in 6 X sodium chloride/sodium
XX citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C
XX to a portion of a nucleotide sequence which encodes a human or murine
XX B lymphocyte antigen (B7-2) extracellular domain. The first peptide has
XX the ability to bind CD28 or CTLA4. The first peptide has an amino acid
XX sequence that is identical or at least 50% identical with the
XX extracellular domain of a human B7-2 peptide (AAB37085). The second
XX peptide is especially an immunoglobulin constant region. This sequence
XX represents the mouse B lymphocyte antigen B7-2. The corresponding nucleic
XX acid is used as a first sequence in the construct of the invention. The
XX nucleic acid are useful in various expression vectors to direct synthesis
XX of the corresponding proteins or peptides in a variety of hosts,
XX particularly eukaryotic cells, e.g. mammalian or insect cell culture. The
XX nucleic acids are also useful for enhancing the immunogenicity of a
XX mammalian cell, e.g. tumour cell (sarcoma) or an antigen presenting cell
XX (macrophage). The fusion proteins or peptides are useful for enhancing
XX or suppressing T cell-mediated immune responses, e.g. in situations of
XX tissue, skin or organ transplantation, or in graft-versus-host disease.
XX The proteins are also useful for enhancing the efficacy of vaccination
XX against a variety of pathogens, and may also be used to upregulate an
XX immune response against a particular pathogen during an infection or
XX against a tumour in a tumour-bearing host.
XX Sequence 309 AA;
XX Query Match 100.0%; Score 1599; DB 21; Length 309;
XX Best Local Similarity 100.0%; Pred. No. 1e-127;
XX Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 MDPRTMGLAIIFFVTLISDAVSVEQAYFNGTAYLPCPTKQNTLSSELVVFQDQ 60
XX Db 1 MDPRTMGLAIIFFVTLISDAVSVEQAYFNGTAYLPCPTKQNTLSSELVVFQDQ 60
XX 61 QKLVLYEHYLGTEKLDSSVNAKYLGRTSFDNRNWTLRHNVQIKDMGSYDCFIQKKPTGS 120
XX
XX Db 61 QKLVLYEHYLGTEKLDSSVNAKYLGRTSFDNRNWTLRHNVQIKDMGSYDCFIQKKPTGS 120
XX Qy 121 IILQOITLTVSVIANFSEPEIKLAQNVTVGNSGINTCTSKQGHKPKKMYFLITNSTNEY 180
XX Db 121 IILQOITLTVSVIANFSEPEIKLAQNVTVGNSGINTCTSKQGHKPKKMYFLITNSTNEY 180
XX Qy 181 GDNWQISQDNNVTLEFSISNLSLSPFDPGVVHMTVVCVLETESMKISSKPLNFTQEFFSPQ 240
XX Db 181 GDNWQISQDNNVTLEFSISNLSLSPFDPGVVHMTVVCVLETESMKISSKPLNFTQEFFSPQ 240
XX Qy 241 TYWKEITASVTVALLVLLIIVCHKKPNQSPSNTASKLERDSNADRETINLKELEPQ 300
XX Db 241 TYWKEITASVTVALLVLLIIVCHKKPNQSPSNTASKLERDSNADRETINLKELEPQ 300
XX Qy 301 IASAKPNAE 309
XX Db 301 IASAKPNAE 309
XX RESULT 4
XX AAR67988
XX ID AAR67988 standard; Protein; 309 AA.
XX AC AAR67988;
XX XX 21-AUG-1995 (first entry)
XX DT Murine B lymphocyte antigen B7-2.
XX XX B lymphocyte antigen; mB7-2.
XX KW Mus musculus.
XX OS
XX FH Key Location/Qualifiers
XX FT Peptide 1..253
XX FT Domain /label= secretory signal peptide
XX FT Domain /label= extracellular
XX FT /note= "Ig superfamily V and C like domains"
XX FT Domain 247..265
XX FT /label= transmembrane domain
XX FT Domain 266..309
XX FT /label= cytoplasmic domain
XX FT Region 40..110
XX FT /label= extracellular
XX FT Region 157..216
XX FT /label= extracellular
XX PN WO9503408-A.
XX XX 02-FEB-1995.
XX PD 26-JUL-1994; 94WO-US08423.
XX PF 26-JUL-1993; 93US-0101624.
XX PR 19-AUG-1993; 93US-0109393.
XX PR 03-NOV-1993; 93US-0147773.
XX XX (DAND ) DANA FARBER CANCER INST INC.
XX PA (REPK ) REPLIGEN CORP.
XX XX Freeman GJ, Gray GS, Greenfield E, Nadler LM;
XX WPI; 1995-0752336/10.
XX DR N-PSDB; AAQ81366.
XX XX Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful
XX PT for enhancing or suppressing T-cell mediated immune responses
XX XX Disclosure; Page 106-107; 175pp; English.
XX XX A cDNA library was constructed in the pCDM8 vector using poly A+

```

CC RNA from activated M12 cells (a murine B cell tumour line).
CC COS cells were transfected with the M12 murine B cell library
CC DNA and screened for expression of B7-2. 6 clones were strongly
CC positive. The B7-2 cDNA insert in clone 4 was sequenced in the
CC pCDM8 expression vector employing the following strategy. Initial
CC sequencing was performed using sequencing primers 17 (AAQ81352) and
CC CDH8R (AAQ8133). DNA sequence obtd. using these primers was used to
CC design additional sequencing primers (see AAQ81367-Q81370). The cycle
CC of sequencing and selection of additional primers was continued
CC until the murine B7-2 cDNA was completely sequenced on both
CC strands. A murine B7-2 clone (mB7-2, clone 4) was obtd.
CC (see AAQ81366/R67988). The predicted protein exhibits many features
CC common to other type I Ig superfamily membrane proteins. Cleavage
CC of the signal peptide would result in a murine B7-2 membrane bound
CC protein having an unmodified mol. wt. of approx. 32 kDa. The
CC extracellular domain contains nine potential N-linked glycosylation
CC sites. Glycosylation may increase the mol. wt. to about 50-70 kDa.
CC E. coli transfected with a vector contg. a cDNA insert encoding
CC mB7-2 clone 4 was deposited with the ATCC on August 18th 1993 as
CC Accession No. 69388.
XX
XX Sequence 309 AA;
XX
XX Query Match 99.6%; Score 1593; DB 16; Length 309;
XX Best Local Similarity 99.7%; Pred. No. 3.4e-127;
XX Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDPRCTMGUAILIFVTVLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSLVVFWQDO 60
DB 1 MDPRCTMGUAILIFVTVLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSLVVFWQDO 60
QY 61 QKLVLYEHLGTEKLDVSNAYLGRGTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGS 120
DB 61 QKLVLYEHLGTEKLDVSNAYLGRGTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGS 120
QY 121 ILLOQTLELSVIANFSEPEIKLAQNVGTGNSGINTCTSKQHPKPKMYFLITNSTNEY 180
DB 121 ILLOQTLELSVIANFSEPEIKLAQNVGTGNSGINTCTSKQHPKPKMYFLITNSTNEY 180
QY 181 GDMNQISQDNVTLELSISLSLSPFDGVVHMTVVCVLETESMKISSKPLNFTQEPSPQ 240
DB 181 GDMNQISQDNVTLELSISLSLSPFDGVVHMTVVCVLETESMKISSKPLNFTQEPSPQ 240
QY 241 TYWKEITASVTVALLLVLLIIVCHKKPNQSPRPSNTASKLERSNADRETINLKELEPQ 300
DB 241 TYWKEITASVTVALLLVLLIIVCHKKPNQSPRPSNTASKLERSNADRETINLKELEPQ 300
QY 301 IASAKPNAE 309
DB 301 IASAKPNAE 309

XX RESULT 5
XX AAR82899
XX ID AAR82899 standard; Protein; 314 AA.
XX AC AAR82899;
XX DT 07-MAY-1996 (first entry)
XX DE Mouse B7-2 alternatively spliced form.
XX KW T-cell costimulatory molecule; B7-2; T-lymphocyte; CD28; CTLA4;
XX receptor; immunoglobulin; signal peptide.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
XX FT Peptide 1..10
XX label= sig_peptide
XX W09523859-A2.
XX PN

PD 08-SEP-1995.
XX
XX 02-MAR-1995; 95WO-US02576.
XX
XX 02-MAR-1994; 94US-0205697.
XX
XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX (DAND) DANA FARBER CANCER INST.
XX
XX Borriello F, Freeman GJ, Nadler LM, Sharpe AH;
XX WPI; 1995-320574/41.
XX N-PSDB; AAT01046.
XX
XX Novel T cell co-stimulatory molecules - corresponding to naturally
XX occurring alternatively spliced forms of T cells co-stimulatory
XX molecules or variants
XX
XX Disclosure; Page 60-61; 111pp; English.
XX
XX A naturally-occurring alternatively spliced form of mouse T-cell
XX co-stimulatory molecule B7-2 (AAR82899) is encoded by exons m1B, 2,
XX 3, 4 and 5 (see AAT01046) of the B7-2 gene. It includes a newly
XX identified alternative signal peptide (AAR82894) encoded by exon
XX m1B (AAT01041). Soluble forms of T-cell costimulatory molecules that
XX include the new signal peptide can be produced. These bind to
XX CD28 or CTLA4 and trigger a costimulatory signal in T-cells.
XX
XX Sequence 314 AA;
XX
XX Query Match 98.6%; Score 1576; DB 16; Length 314;
XX Best Local Similarity 100.0%; Pred. No. 9.6e-126;
XX Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CTWGLAILFVTVLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSLVVFWQDOOKLV 64
DB 10 CTWGLAILFVTVLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSLVVFWQDOOKLV 69
QY 65 LYEHLGTEKLDVSNAYLGRGTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGSIIQ 124
DB 70 LYEHLGTEKLDVSNAYLGRGTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGSIIQ 129
QY 125 QTUTEISVTANFSEPEIKLAQNVGTGNSGINTCTSKQHPKPKMYFLITNSTNEYGDM 184
DB 130 QTUTEISVTANFSEPEIKLAQNVGTGNSGINTCTSKQHPKPKMYFLITNSTNEYGDM 189
QY 185 QISQDNVTLELSISLSLSPFDGVVHMTVVCVLETESMKISSKPLNFTQEPSPQTYWK 244
DB 190 QISQDNVTLELSISLSLSPFDGVVHMTVVCVLETESMKISSKPLNFTQEPSPQTYWK 249
QY 245 EITASVTVALLLVLLIIVCHKKPNQSPRPSNTASKLERSNADRETINLKELEPQASA 304
DB 250 EITASVTVALLLVLLIIVCHKKPNQSPRPSNTASKLERSNADRETINLKELEPQASA 309
QY 305 KPAE 309
DB 310 KPAE 314

XX RESULT 6
XX AAY44414
XX ID AAY44414 standard; protein; 358 AA.
XX AC AAY44414;
XX DT 22-MAR-2000 (first entry)
XX DE B7.2-beta 2 microglobulin fusion protein-2.
XX KW B7.2-b2m fusion protein; murine B7.2 co-stimulatory molecule; b2m;
XX human beta-2 microglobulin; tumour antigen; bacterial antigen;
XX viral antigen; tumour-specific cytotoxic T-cell; vaccination;
XX immune therapy.


```

XX OS Mus sp.
XX OS Homo sapiens.
XX FH Key
XX FH Peptide
XX FT Location/Qualifiers
XX FT 1..20
XX FT /label= Signal peptide
XX FT /note= "Derived from human beta-2 microglobulin"
XX FT 21..239
XX FT /note= "Extracellular portion of murine B7-2"
XX FT 240..244
XX FT /note= "Sequence created by insertion of restriction site
XX FT in the nucleic acid sequence"
XX FT 245..249
XX FT /label= linker_sequence
XX FT 260..358
XX FT /note= "Mature form of human beta-2 microglobulin"
XX FT
XX FT WO9964597-A1.
XX PN
XX XX
XX PD 16-DEC-1999.
XX XX
XX PF 03-JUN-1999; 99WO-US12309.
XX XX
XX PR 10-JUN-1999; 98US-0088813.
XX XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX XX
XX PI Ribaudo RK, Shields M;
XX XX WPI; 2000-116544/10.
XX DR
XX XX New beta-2 microglobulin fusion proteins, used for the preparation of
XX PT vaccines for use against bacterial antigens -
XX PS Claim 15; Fig 4; 49pp; English.
XX CC The present sequence is a B7.2-b2m fusion protein having the hbeta-2
XX CC signal sequence. The fusion protein comprises murine B7.2 co-stimulatory
XX CC molecule and mature human beta-2 microglobulin. Signal peptides directs
XX CC expression of the protein to a specified location in the cell. The
XX CC presence of fusion protein on the tumour cell surface enhances the immune
XX CC system response to the tumour antigens present on tumour cell surface by
XX CC boosting the generation of tumour-specific cytotoxic T-cells. These
XX CC proteins can effectively target a desired protein to the outer membrane
XX CC of a cell. The proteins and corresponding nucleic acids encoding them can
XX CC be used for vaccination against bacterial, viral or tumour antigens. The
XX CC products can also be used for immune therapy.
XX SQ Sequence 358 AA;
XX Query Match 73.3%; Score 1172.5; DB 21; Length 358;
XX Best Local Similarity 94.1%; Pred. No. 2.3e-91;
XX Matches 224; Conservative 8; Mismatches 5; Indels 1; Gaps 1;
Qy 6 TMGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPTKAQNISLSLVVFWQDQQLVL 65
Db 4 SVALAVLALLSLUGL-EAVSVETQAYFNGTAYLPCPTKAQNISLSLVVFWQDQQLVL 62
Qy 66 YEHYLGTEKLDVSNARYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGSIILQ 125
Db 63 YEHYLGTEKLDVSNARYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGSIILQ 122
Qy 126 TLTELSVIANFSEPEIKLAQNVGTNSGINLTCTSKQGHKPKMYFLITNSTNEYGNMQ 185
Db 123 TLTELSVIANFSEPEIKLAQNVGTNSGINLTCTSKQGHKPKMYFLITNSTNEYGNMQ 182
Qy 186 ISQDNVTELSFISNSLSLSPFDGVVHMTVCVLETESMKISSKPLNFTQEPFSPQTYW 243
Db 183 ISQDNVTELSFISNSLSLSPFDGVVHMTVCVLETESMKISSKPLNFTQEPFSPQTYW 240
RESULT 7

```

```

AAV44413
ID AAY44413 standard; protein; 339 AA.
XX AC AAY44413;
XX DT 22-MAR-2000 (first entry)
XX DE B7.2-beta 2 microglobulin fusion protein-1.
XX KW B7.2-b2m fusion protein; murine B7.2 co-stimulatory molecule; b2m;
XX KW human beta-2 microglobulin; tumour antigen; bacterial antigen;
XX KW viral antigen; tumour-specific cytotoxic T-cell; vaccination;
XX KW immune therapy.
XX OS Mus sp.
XX OS Homo sapiens.
XX FH Key
XX FH Domain
XX FT Location/Qualifiers
XX FT 2..220
XX FT /note= "Extracellular portion of murine B7.2"
XX FT 221..225
XX FT /note= "Sequence created by insertion of restriction site
XX FT in the nucleic acid sequence"
XX FT 226..240
XX FT /note= "linker sequence"
XX FT 241..339
XX FT /note= "Mature form of human beta-2 microglobulin"
XX PN WO9964597-A1.
XX PD 16-DEC-1999.
XX PF 03-JUN-1999; 99WO-US12309.
XX PR 10-JUN-1998; 98US-0088813.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Ribaudo RK, Shields M;
XX DR WPI; 2000-116544/10.
XX XX New beta-2 microglobulin fusion proteins, used for the preparation of
XX PT vaccines for use against bacterial antigens -
XX PS Claim 15; Fig 3; 49pp; English.
XX CC The present sequence is a B7.2- b2m fusion protein comprising murine B7.2
XX CC co-stimulatory molecule and mature human beta-2 microglobulin. The
XX CC presence of fusion protein on the tumour cell surface enhances the immune
XX CC system response to the tumour antigens present on tumour cell surface by
XX CC boosting the generation of tumour-specific cytotoxic T-cells. These
XX CC proteins can effectively target a desired protein to the outer membrane
XX CC of a cell. The proteins and corresponding nucleic acids encoding them can
XX CC be used for vaccination against bacterial, viral or tumour antigens. The
XX CC products can also be used for immune therapy.
XX SQ Sequence 339 AA;
XX Query Match 72.7%; Score 1162; DB 21; Length 339;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-90;
XX Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 24 VSVETQAYFNGTAYLPCPTKAQNISLSLVVFWQDQQLVLYEHYLGTEKLDVSNARYL 83
Db 2 VSVETQAYFNGTAYLPCPTKAQNISLSLVVFWQDQQLVLYEHYLGTEKLDVSNARYL 61
Qy 84 GRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGSIILQOTLTLSLVIANFSEPEIKL 143
Db 62 GRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGSIILQOTLTLSLVIANFSEPEIKL 121
Qy 144 AQNVGTNSGINLTCTSKQGHKPKMYFLITNSTNEYGNMQISQDNVTELSFISNSLSL 203

```

```
Db 122 AONVTGNSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNMQISQDNVTFLSFISLSL 181
QY 204 SFDGVVHMTVVCVLETESMKISSKPLNFTOEPFSPQTYW 243
Db 182 SFDGVVHMTVVCVLETESMKISSKPLNFTOEPFSPQTYW 221

RESULT 8
AAW34452
ID AAW34452 standard; protein; 313 AA.
XX
AC AAW34452;
XX
DT 09-MAR-1998 (first entry)
XX
DE Rat CD86.
XX
KW CD86; rat; immunosuppression; organ transplantation; therapy.
XX
OS Rattus rattus.
XX
PN JP09291100-A.
XX
PD 11-NOV-1997.
XX
PF 24-APR-1996; 96JP-0102554.
XX
PR 24-APR-1996; 96JP-0102554.
XX
PA (SUMS ) SUMITOMO ELECTRIC IND CO.
XX
DR WPI; 1998-037055/04.
DR N-PSDB; AAT99926.
XX
Rat CD86, its gene and antibody against it - used in
immunosuppression and organ transplantation treatment
XX
Claim 1; Page 10-11; 13pp; Japanese.
XX
This sequence represents the rat CD86 protein. This polypeptide can be
used to give a new form of immunosuppression and organ transplantation
treatment. Antisense sequences targeted against the DNA encoding this
sequence, and antibodies specific for this sequence can be used
similarly.
XX
SQ Sequence 313 AA;

Query Match 64.2%; Score 1027; DB 19; Length 313;
Best Local Similarity 68.6%; Pred. No. 4.6e-79;
Matches 210; Conservative 29; Mismatches 53; Indels 14; Gaps 5;

QY 5 CTWGLAIFVTVLLISDAVSVETOAVFNGTAYLPCPTKAONLSLSLVFWQDOOKLY 64
Db 10 CTWYLGILFSLVAILLSDAVPVVRQAYFNSTAYLPCPTKAONISPSLVFWQDRKXSV 69

QY 65 LYEHVLTGKLDVSNVAKYLGRTSFDNRNWTLRHNVQIKDMGSDYDFIQKPPGTGSIILQ 124
Db 70 LYEHVLTGAEKLDVSNVAKYLGRTSFDNRNQAALRHNVQIKDGTGLYDFIQKPTGSIILQ 129

QY 125 QLTLELSVIANFSPPEIKLAQNTVGTNSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNM 184
Db 130 QWETELSVIANFSEPEIEEAQNTRNIGNLTCSSKQGYPRPTKMYFLITNSTNEYGDNM 189

QY 185 QISQDNVTFLSFISLSLSLSPDGVVHMTVVCVLETESMKISSKPLNFTOEPFSPQ--T 241
Db 190 QISQDNVTFLSFISLSLSLSPDGVVHMTVVCVLETESMKISSKPLNF--FSQPFDRK 247

QY 242 YNKEITASVTVALLLVMLLIIV-----CHKPNQPSRPSNTASKLERDSNADRETINIK 295
Db 248 TWIQIAG--PSSLICCLFLVVYKAVKCLRMQNGPRSPKTKCESQKDSGVD--ESINLE 304

QY 296 ELEPQI 301
|:|:|:
```

```
Db 305 EVEPQL 310

RESULT 9
AAR67984
ID AAR67984 standard; Protein; 329 AA.
XX
AC AAR67984;
XX
DT 20-AUG-1995 (first entry)
XX
DE Human B lymphocyte antigen B7-2 predicted from clone 29.
XX
KW CTLA4/CD28; counter receptor; B lymphocyte antigen; B7-2.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT Domain 24..245
FT /label= secretory signal peptide
FT /label= extracellular Ig superfamily.V-& C-like
FT /note= "claimed"
FT Domain 246..268
FT /label= hydrophobic transmembrane domain
FT Domain 269..329
FT /label= cytoplasmic domain
FT Domain 40..110
FT /label= Ig-like domain
FT Domain 157..218
FT /label= Ig-like domain
FT Region 81..89
FT /label= CTLA4 or CD28 binding sequence
FT Region 188-200
FT /label= CTLA4 or CD28 binding sequence
FT Domain 269-282
FT /note= "probably involved in intracellular signalling"
XX
WO9503408-A.
XX
PD 02-FEB-1995.
XX
PF 26-JUL-1994; 94WO-US08423.
XX
PR 26-JUL-1993; 93US-0101624.
PR 19-AUG-1993; 93US-0109393.
PR 03-NOV-1993; 93US-0147773.
XX
PA (DAND ) DANA FARBER CANCER INST INC.
PA (REPK ) REPLIGEN CORP.
XX
Freeman GJ, Gray GS, Greenfield E, Nadler LM;
XX
WPI; 1995-075236/10.
XX N-PSDB; AAQ81351.
XX
Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful
for enhancing or suppressing T-cell mediated immune responses
XX
Claim 35; Fig 8; 175pp; English.
XX
A cDNA library was constructed in the pCDM8 vector using poly A+ RNA
from the human anti-IGM activated B cells. Four clones were strongly
positive for B7-2 expression by indirect immunofluorescence using
CTLA4lg and flow cytometric analysis. The B7-2 cDNA insert in clone
29 was sequenced in the pCDM8 expression vector employing the
following strategy. Initial cloning was performed using
sequencing primers T7 (AAQ81352), CDM8R (AAQ81353) (Invitrogen)
homologous to pCDM8 vector sequences adjacent to the clone B7-2 cDNA.
Cloning was performed using dye terminator chemistry and an ABI
automated DNA sequencer. DNA sequence obtd. using these primers was used
to design additional sequencing primers (see AAQ81354-Q81363). This cycle
```

CC of sequencing and selection of additional primers was continued until
 CC the B7-2 cDNA was completely sequenced on both strands. The human
 CC B7-2 clone 29 cDNA sequence is given in A081351. The predicted
 CC protein sequence (AAR67994) exhibits many features common to other
 CC type 1 Ig superfamily membrane proteins. Following cleavage of the
 CC signal peptide the resulting membrane-bound protein would have an
 CC unmodified mol. wt. of approx. 34 kDa. The extracellular domain
 CC contains eight potential N-linked glycosylation sites. E. coli
 CC transfected with a vector contg. the cDNA insert of clone 29 was
 CC deposited under ATCC 69357 on July 26 1993.
 XX
 SQ Sequence 329 AA;

Query Match 46.5%; Score 743.5; DB 16; Length 329;
 Best Local Similarity 51.5%; Pred. No. 6.3e-55;
 Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

Qy 1 MDPRCTMGLAILFVTVLLISDAVSVEYQAYNGTAYLPCPTTKAQNISSELVFWQDQ 60
 Db 1 MDPCQTMGLSNILFVMAFLSLGAPLKIQAYFNETADLPQFANSQNSSELVFWQDQ 60
 Qy 61 QKLVLVHYLGTPEKLDVSNAYKLGRTSFDNRNNTLRLHNVQIKDMSYDCFIQKKPPTGS 120
 Db 61 ENLVLENVYLGKEKFDVSHVSGMRTSFDSDSWTLRLHNLQIKDGLYQCIIHHKKPTGM 120
 Qy 121 IILQOTLTELSEVIANSEPEIKLAQNVGTGNSGINTCTSKOHPKPKMYFLI--TNSTN 178
 Db 121 IRIHQNSLSLVANFSPEIVPISNITENVYINLTCSIHGYPEPKMSVLLRTKNTI 180
 Qy 179 EYGDNNQISQDNNVTELSISLSLSPDGVGHMTVVCLETESMKISSKPLNFTOEPPS 238
 Db 181 EYDGIWQSDNNVTELYDVSISLSVSPDVTNSMTIFCILETDKTRLLSSPFSIELEDQ 240
 Qy 239 P---QTYWKEITASTVALLVWL--LIIVCHKKNQSRP-----SNTASKLRDSNADR 289
 Db 241 PPPDHIPW--ITAVLPTVILICVMFCLILMKWKKKRPNSYKCGTNTMERSEQTKKR 298
 Qy 290 ETINLKE 296
 Db 299 EKIHPE 305

RESULT 10
 AAW08467
 ID AAW08467 standard; Protein; 329 AA.

XX
 AC AAW08467;

XX
 DT 08-APR-1997 (first entry)

XX
 DE Human B lymphocyte antigen B7-2.

XX
 KW CTLA4; CD28; ligand; B7-2; B lymphocyte antigen; B-cell;
 KW costimulation; immunoglobulin; antibody; autoimmune disease;
 KW allergy; tumour; vaccine; graft versus host disease; T-cell;
 KW T lymphocyte; TH2 response; immunosuppressive; immunostimulant;
 KW therapy.

XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers

FT Peptide 1..13

FT Protein /label= sig_peptide 24..329

FT Domain /label= Mat_protein 24..245

FT /label= Extracellular_domain

FT /note= "extracellular Ig superfamily V and C-like domain"

FT Region 40..110

FT /label= Ig-like_domain 157..218

FT Region /label= Ig-like_domain

FT Binding-site 81..89
 FT label= CTLA4/CD28_binding_site
 FT 188..200
 FT Binding-site
 FT label= CTLA4/CD28_binding_site
 FT 24..133
 FT Region
 FT /label= Variable_region
 FT /note= "(Claim 42)"
 FT 134..235
 FT Region
 FT /label= Constant_region
 FT 246..268
 FT Domain
 FT /label= Transmembrane_domain
 FT 269..329
 FT Domain
 FT /label= Cytoplasmic_domain
 FT 268..282
 FT Region
 FT /note= "region probably involved in intracellular signalling"
 FT 33
 FT Modified-site
 FT /label= Glycosylation
 FT /note= "putative N-glycosylation site"
 FT 47
 FT Modified-site
 FT /label= Glycosylation
 FT /note= "putative N-glycosylation site"
 FT 135
 FT Modified-site
 FT /label= Glycosylation
 FT /note= "putative N-glycosylation site"
 FT 146
 FT Modified-site
 FT /label= Glycosylation
 FT /note= "putative N-glycosylation site"
 FT 154
 FT Modified-site
 FT /label= Glycosylation
 FT /note= "putative N-glycosylation site"
 FT 177
 FT Modified-site
 FT /label= Glycosylation
 FT /note= "putative N-glycosylation site"
 FT 213
 FT Modified-site
 FT /label= Glycosylation
 FT /note= "putative N-glycosylation site"
 FT
 XX WO9640915-A2.
 XX
 XX 19-DEC-1996.
 XX
 XX 06-JUN-1996; 96WO-US09052.
 XX
 XX 07-JUN-1995; 95US-0479744.
 XX
 XX (DAND) DANA FARBER CANCER INST INC.
 XX (REPK) REPLIGEN CORP.
 XX
 XX Freeman GJ, Gray GS, Nadler LM;
 XX
 XX WPI, 1997-077269/07.
 XX N-PSDB; AAT49181.
 XX
 XX DNA encoding a B7-2 fusion protein - used to enhance or down
 XX regulate B lymphocyte antigens
 XX
 XX Claim 4; Page 95-96; 171pp; English.
 XX
 XX Human B-lymphocyte antigen B7-2 (AAW08467) is a CTLA4/CD28 ligand
 XX which costimulates T cell activation. It shows 26% amino acid
 XX identity to human B7-1. Its sequence was deduced from a cDNA
 XX clone (AAT49181) isolated from an anti-IgM activated B cell cDNA
 XX library. Novel fusion proteins comprising the extracellular domain,
 XX variable region-like or constant region-like domains of B7-2 (see
 XX also AAW08472-73) and e.g. an immunoglobulin heavy chain constant
 XX region can be expressed in host cells and used to enhance or
 XX suppress T cell-mediated immune responses.
 XX
 SQ Sequence 329 AA;

Query Match 46.5%; Score 743.5; DB 18; Length 329;
 Best Local Similarity 51.5%; Pred. No. 6.3e-55;

peptide, and a second nucleotide sequence encoding a second peptide.
The first nucleotide sequence hybridizes in 6 X sodium chloride/sodium citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C to a portion of a nucleotide sequence which encodes a human or murine B lymphocyte antigen (B7-2) extracellular domain. The first peptide has the ability to bind CD28 or CTLA4. The first peptide has an amino acid sequence that is identical or at least 50% identical with the extracellular domain of a human B7-2 peptide (AAB37085). The second peptide is especially an immunoglobulin constant region. This sequence represents the human B lymphocyte antigen B7-2 encoded by the human B7-2 clone 29 cDNA. The nucleic acid is used as a first sequence in the construct of the invention. The nucleic acid are useful in various expression vectors to direct synthesis of the corresponding proteins or peptides in a variety of hosts, particularly eukaryotic cells, e.g. mammalian or insect cell culture. The nucleic acids are also useful for enhancing the immunogenicity of a mammalian cell, e.g. tumour cell (sarcoma) or an antigen presenting cell (macrophage). The fusion proteins or peptides are useful for enhancing or suppressing T cell-mediated immune responses, e.g. in situations of tissue, skin or organ transplantation, or in graft-versus-host disease. The proteins are also useful for enhancing the efficacy of vaccination against a variety of pathogens, and may also be used to upregulate an immune response against a particular pathogen during an infection or against a tumour in a tumour-bearing host.

XX Sequence 329 AA;

Query Match 46.5%; Score 743.5; DB 21; Length 329;
Best Local Similarity 51.5%; Pred. No. 6.3e-55;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;
QY 1 MDPRTMGLAILFVTVLLISDAVSVEVETQAYFNGTAYLPCPFTKAQNISLSLVVFWQDQ 60
DB 1 MDPQCTMGLSNILFWMAFLLSGAAPLKIQAYFNETADLPQCFANSQNSLSLVVFWQDQ 60
QY 61 QKLVLYEHVLTGTEKLDVSNVAKYLGRTSFDNRNWTLRHNVQIKDMGSDYCFIQKKPTGS 120
DB 61 ENLVINEVLYGKEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIILHKKPTGM 120
QY 121 IILQOQTUTELSVIANFSEPEIKLAQNTVGTSGINLTCTSKQGHKPKKMYFLI--TNSTN 178
DB 121 IRIHQNSLSVLANSFQSEIPIVPSINITENVYINLTCSIHGYPPKMSVLLRTKNSIT 180
QY 179 EYGDNMQISQDNVTLEFISLSLSLSPDPGVWHTVVCVLETESMKISSKPLNFTQEPFS 238
DB 181 EYDGIMQKSDNVTELYDVSLVSLSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDPO 240
QY 239 P---QTYWKEITASVTVALLLVMI--LIIIVCHKKPNQSRP----SNTASKLERDSNADR 289
DB 241 PPPDHIPW--ITAVLPTVVICVMYFCILILWKKKKRPNSYKCTNTMERESSEQTKKR 298
QY 290 ETINLXE 296
DB 299 EKIHPIE 305

RESULT 13
AAE14634
ID AAE14634 standard; Protein; 329 AA.
XX AAE14634;
AC AAE14634;
XX

16-JUL-2002 (first entry)

Human B7-2 protein.

T cell; CD3; accessory molecule; CD28; cancer; infectious disease;
immunotherapy; human immunodeficiency virus; HIV infection;
cytokine; human; B7-2; CD86.

OS Homo sapiens.
XX US6352694-B1.
PN

XX 05-MAR-2002.
PD
XX 10-MAR-1995; 95US-0403253.
PF
XX 03-JUN-1994; 94US-0253964.
PR
XX (GENM) GENETICS INST INC.
PA (UNMI) UNIV MICHIGAN.
XX
XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
PI WPI; 2002-314696/35.
XX N-PSDB; AAD27968.
DR
XX Inducing T cell population to proliferate, useful in cancer therapy,
PT comprises activating T cells by contacting T cells in vitro with
PT immobilized anti-CD3 antibody and stimulating accessory molecule on T
PT cell surface -
XX

XX Example 11; Column 63-66; 71pp; English.

XX The invention relates to a method of inducing T cell population to
XX proliferate for use in therapy comprising activating T cells by
XX contacting T cells in vitro with anti-CD3 antibody which is immobilised
XX on solid phase surface, and stimulating accessory molecule on T cell
XX surface in vitro with anti-CD28 antibody, or stimulatory form of
XX natural ligand for CD28 such as B7-1 or B7-2. The method is useful
XX for inducing a population of T cells to proliferate in sufficient
XX numbers for use in therapy e.g., for treating cancer or an infectious
XX disease. The method can be used to selectively expand the
XX population of CD28⁺, CD4⁺, CD8⁺, CD28RA⁺ or CD28RO⁺ T cells for
XX immunotherapy. The T cell population resulting by the method can be
XX genetically transduced and used for immunotherapy or can be used for in
XX vitro analysis of infectious agents such as human immunodeficiency
XX virus (HIV). Proliferation of a population of CD4⁺ T cells obtained
XX from an individual infected with HIV can be achieved and the cells
XX rendered resistant to HIV infection. Following the expansion of the T
XX cells to sufficient numbers, the expanded T cells are restored to the
XX individual. Also CD4⁺ T cells expanded by the above mentioned is
XX useful for treating HIV infection in an individual. A population
XX of tumour-infiltrating lymphocytes can be obtained from an individual
XX afflicted with cancer and the T cells stimulated to proliferate to
XX sufficient numbers and restored to the individual. The supernatants from
XX cultures of T cells expanded from above mentioned method are useful as a
XX rich source of cytokines and can be used to sustain T cells in vivo or
XX ex vivo. Stimulating and expanding a population of antigen specific
XX T cells are useful in therapeutic conditions where it is desirable to
XX upregulate an immune response. The T cell proliferation occurs in
XX the absence of exogenous growth factors or accessory cells. The present
XX sequence is human B7-2 (CD86) protein used in the invention.

XX Sequence 329 AA;

Query Match 46.5%; Score 743.5; DB 23; Length 329;
Best Local Similarity 51.5%; Pred. No. 6.3e-55;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;
QY 1 MDPRTMGLAILFVTVLLISDAVSVEVETQAYFNGTAYLPCPFTKAQNISLSLVVFWQDQ 60
DB 1 MDPQCTMGLSNILFWMAFLLSGAAPLKIQAYFNETADLPQCFANSQNSLSLVVFWQDQ 60
QY 61 QKLVLYEHVLTGTEKLDVSNVAKYLGRTSFDNRNWTLRHNVQIKDMGSDYCFIQKKPTGS 120
DB 61 ENLVINEVLYGKEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIILHKKPTGM 120
QY 121 IILQOQTUTELSVIANFSEPEIKLAQNTVGTSGINLTCTSKQGHKPKKMYFLI--TNSTN 178
DB 121 IRIHQNSLSVLANSFQSEIPIVPSINITENVYINLTCSIHGYPPKMSVLLRTKNSIT 180
QY 179 EYGDNMQISQDNVTLEFISLSLSLSPDPGVWHTVVCVLETESMKISSKPLNFTQEPFS 238
DB 181 EYDGIMQKSDNVTELYDVSLVSLSPDPVTSNMTIFCILETDKTRLLSSPFSIELEDPO 240

Qy 239 P---QTYWKEITASVTVALLLVML--LIIVCHKKPNQSRP-----SNTASKLERDSNADR 289
 Db 241 PPPDHIPW--ITAVLPTVICWVFCLLIWKWKKKRPNSYKCGTNTMEREESEQTKKR 298
 Qy 290 ETINLXE 296
 Db 299 EKIHPIE 305
 RESULT 14
 AAW14944
 ID AAW14944 standard; Protein; 250 AA.
 XX
 AC AAW14944;
 XX
 DT 16-JUN-1997 (first entry)
 XX
 DE Chimeric human/porcine CD86.
 XX
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW CD68; monoclonal antibody; chimeric antibody; diagnosis.
 XX
 OS Chimeric Homo sapiens;
 OS Chimeric Sus scrofa.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= Sig_peptide
 FT Protein 26..250
 FT /label= Mat_protein
 FT Region 246..250
 FT /label= Histidine_tag
 XX
 PN WO9711971-A1.
 XX
 PD 03-APR-1997.
 XX
 PF 27-SEP-1996; 96WO-US5575.
 XX
 PR 26-SEP-1996; 96US-0004489.
 PR 28-SEP-1995; 95US-0004489.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 XX
 DR WPI; 1997-212855/19.
 DR N-PSDB; AAT62939.
 XX
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 XX
 PS Disclosure; Page 69-70; 105pp; English.
 XX
 CC A chimeric human/porcine CD86 (B7-2) cell adhesion molecule has
 CC amino acid residues 1-4 and 197-245 from human CD86, and amino
 CC acids 5-196 from porcine CD86. It is encoded by a DNA construct
 CC (AAT62939) obtd. by PCR amplification of porcine sequences and
 CC ligation to a sequence encoding the C-terminal region of human
 CC CD86 IgC domain. A signal sequence facilitates efficient
 CC secretion from transfected mammalian cells. Antibodies to porcine
 CC CD86 protein, P-selectin (see also AAW14931-42) and vascular cell
 CC adhesion molecule (see also AAW14931-42) are useful for diagnosing
 CC human rejection of porcine xenotransplants and for improving
 CC xenotransplantation of porcine cells, tissues and organs into human
 CC recipients.
 XX
 SQ Sequence 250 AA;
 Query Match 44.9%; Score 718; DB 18; Length 250;

Best Local Similarity 57.7%; Pred. No. 6.3e-53;
 Matches 139; Conservative 38; Mismatches 62; Indels 1;
 Qy 1 MDRCTMGALILFVTVLLISDAVSQAYFNGTAYLPCFPTKAQNLSELVVFWDQ 60
 Db 1 MDPOCTMGLRNILVGMVLLSQAASLSKQAYFNETGELPCHFTNSQNLSELVVFWDQ 60
 Qy 61 QKLVLYEHLGTEKLDSSVNAKYLQRTSFRNNWTLRLHNVOIKDMGSYDCFIQKPPPTGS 120
 Db 61 DNLVLYELRGQEKPHNVNSKYMGRTSFDQATWTLRLHNVOIKDKGSYQCFIHHKPGHL 120
 Qy 121 IILQOTLTLSLVIANFSPEIKLAQNVGTGNSGJNLCTSKQGHKPKKMYFLIT--NSTN 178
 Db 121 VPIHQMSDLSVLNFSQPEINLLTNHTENSVINLTCSSSTQGPPEPQMYMLLTKNSTT 180
 Qy 179 EYGDNMQIISQDNVTSLFISNSLSLSPFDGVMHMTVVCVLETESMKISKPLNFTQEPFS 238
 Db 181 EHDADMKKSQDNVTSLYDVSISLSVSPDVTNMTIFCILETDKTRLLSSPFSIELEDPQ 240
 Qy 239 P 239
 Db 241 P 241
 RESULT 15
 AAR71478
 ID AAR71478 standard; Protein; 323 AA.
 XX
 AC AAR71478;
 XX
 DT 09-OCT-1995 (first entry)
 XX
 DE B70 type B antigen which binds CTLA-4 and CD28.
 XX
 KW B70 antigen; CTLA-4; CD28; T cell response.
 OS Homo sapiens.
 XX
 PN WO9506738-A.
 XX
 PD 09-MAR-1995.
 XX
 PF 02-SEP-1994; 94WO-US09642.
 XX
 PR 03-SEP-1993; 93US-0116882.
 PR 13-SEP-1993; 93US-0120606.
 XX
 PA (AZUM/) AZUMA M.
 PA (OKUM/) OKUMURA K.
 PA (SCHE) SCHERING CORP.
 XX
 PI Azuma M, Lanier LL, Okumura K, Phillips JH;
 PI Somoza Diaz-Sarmiento M;
 XX
 DR WPI; 1995-115453/15.
 DR N-PSDB; AAQ85873.
 XX
 PT New CTLA-4/CD28 binding protein, B70 - used to develop prods for
 PT modulating the physiology, growth or development of cells.
 XX
 PS Claim 3; Page 44-45; 55pp; English.
 XX
 CC B70 is a natural proteinaceous binding partner for CTLA-4 and CD28
 CC markers/antigens. It is distinct from the known B7/BBI marker. It is
 CC representative of 'type B' markers/antigens/binding partners. The
 CC type A markers/binding partners include both CTLA-4 and CD28 and
 CC antibodies specific for B70, and are characterised, in part, by the
 CC property of serving as a binding partner for B70. A cDNA encoding a
 CC B70 antigen was cloned by expression cloning using mAb 1f2.236 to
 CC select COS7 cells transfected with a cDNA library cloned into the
 CC pJFE14 vector. The library was made from RNA isolated from a human
 CC EBV-transformed B-lymphoblastoid cell line JY.

SQ Sequence 323 AA;

Query Match 44.4%; Score 710.5; DB 16; Length 323;

Query Match 44.4%; Score 10.5; DB 18; Length 323;
Best Local Similarity 50.8%; Pred. No. 3.9e-52;
Matches 153; Conservative 44; Mismatches 91; Indels 13; Gaps 5;

QY 7 MGLAILIFVTVLLISDAVSVEQTAYFNGTAYLPCPFTKAQNISLSSELVFWQDQQKLVLV 66

Db 1 MGLSNILFVMAFLLSGGAAPLKIQAYFNETADLPFCOFANSONQSLSELVTFWQDQENLVN 60

QY 67 EHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGYDCFIQKKPPTGSIILQQT 126

61 EVYLGEKEFDSVHSKYMGRTSFSDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRHOM 120

QY 127 LTEL SVIANF SEPEIK LAQNV TNSGIN LTCTSK QGHPKPKMYFLI -- TNSTNEYGDNM 184

Db 121 NSELSVLANFQSPEIPIPSINITENVYINLTCSIIHGYPKQMSVLLRTKNSTIEYDGM 180

QY 185 QISQDNVTELFISNSLSLSPDPGVWHMTVVCVLETESMKISSKPLNFTQEEFSP--QT 241

181 QKSDQNTELYDVISLSVSFPDVTGNMTFCILETDKTRLLSSPFSIELEDPQPPDHI 240

QY 242 YWKEITASVTVALLVML--LIIVCHKPNQPSRP-----SNTASKLERDSNADRETINLK 295

241 PW--ITAVLPTVICVMVFCLWKKKKRPNRSYKCGTNTMERISEOTKKREKIHLP 298

Ov 296 E 296

—

Search completed: February 13, 2003, 11:30:59
Job time : 33.4498 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 11:32:49 ; Search time 16.9514 Seconds
(without alignments)
465.720 Million cell updates/sec

Title: US-09-425-516-23

Perfect score: 1599

Sequence: 1 MDPRTWGLAIFVTVLLI.....ETINLKELEPQIASAKPNAE 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/ECT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/ECTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1599	100.0	309	9 US-09-441-411-13	Sequence 13, Appl
2	1599	100.0	309	9 US-09-441-411-18	Sequence 18, Appl
3	1599	100.0	309	9 US-09-441-411-24	Sequence 24, Appl
4	1599	100.0	309	10 US-09-837-867A-21	Sequence 21, Appl
5	1576	98.6	314	9 US-09-441-411-14	Sequence 14, Appl
6	1576	98.6	314	9 US-09-441-411-19	Sequence 19, Appl
7	1576	98.6	314	10 US-09-837-867A-13	Sequence 13, Appl
8	1567	98.0	356	9 US-09-441-411-11	Sequence 11, Appl
9	1567	98.0	356	9 US-09-441-411-12	Sequence 12, Appl
10	1567	98.0	356	9 US-09-441-411-16	Sequence 16, Appl
11	1567	98.0	356	9 US-09-441-411-17	Sequence 17, Appl
12	1562	97.7	303	9 US-09-441-411-15	Sequence 15, Appl
13	1562	97.7	303	9 US-09-441-411-20	Sequence 20, Appl
14	743.5	46.5	329	8 US-08-592-711-4	Sequence 4, Appl
15	743.5	46.5	329	9 US-09-441-411-26	Sequence 26, Appl
16	743.5	46.5	329	10 US-09-837-867A-23	Sequence 23, Appl
17	710.5	44.4	323	9 US-09-896-738-11	Sequence 11, Appl
18	710.5	44.4	323	9 US-09-915-789A-16	Sequence 16, Appl
19	710.5	44.4	323	9 US-09-441-411-22	Sequence 22, Appl

20	710.5	44.4	323	10	US-09-955-866-5	Sequence 5, Appli
21	710	44.4	324	10	US-09-910-174A-6	Sequence 6, Appli
22	707	44.2	260	10	US-09-845-899A-5	Sequence 5, Appli
23	674	42.2	351	10	US-09-756-983-18	Sequence 18, Appl
24	640.5	40.1	329	10	US-09-303-510-6	Sequence 6, Appli
25	640.5	40.1	329	10	US-09-303-040-6	Sequence 6, Appli
26	635	39.7	219	9	US-09-915-789A-22	Sequence 22, Appli
27	230	14.2	45	10	US-09-837-867A-30	Sequence 30, Appl
28	227.5	14.2	306	10	US-09-837-867A-17	Sequence 17, Appl
29	215.5	13.5	315	10	US-09-910-174A-28	Sequence 28, Appl
30	212	13.3	320	10	US-09-837-867A-2	Sequence 2, Appli
31	182	11.4	302	9	US-09-896-738-13	Sequence 13, Appl
32	182	11.4	302	9	US-09-915-789A-18	Sequence 18, Appl
33	182	11.4	302	10	US-09-789-561-136	Sequence 136, App
34	182	11.4	302	10	US-09-955-866-7	Sequence 7, Appli
35	182	11.4	309	10	US-09-910-174A-7	Sequence 7, Appli
36	182	11.4	316	10	US-09-875-338-11	Sequence 11, Appl
37	182	11.4	343	10	US-09-764-853-630	Sequence 630, App
38	182	11.4	344	10	US-09-764-853-812	Sequence 812, App
39	182	11.4	345	10	US-09-764-853-810	Sequence 810, App
40	182	11.4	534	10	US-09-875-338-7	Sequence 7, Appli
41	181	11.3	316	9	US-09-790-622-4	Sequence 4, Appli
42	181	11.3	316	10	US-09-789-561-135	Sequence 135, App
43	180	11.3	316	9	US-09-978-295A-137	Sequence 137, App
44	180	11.3	316	9	US-09-896-738-14	Sequence 14, Appl
45	180	11.3	316	9	US-09-978-697-137	Sequence 137, App

ALIGNMENTS

RESULT 1
US-09-441-411-13
; Sequence 13, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441.411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-13

Query Match 100.0%; Score 1599; DB 9; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.7e-119;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDPRTWGLAIFVTVLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLVWFWDQ 60
Db	1	MDPRTWGLAIFVTVLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLVWFWDQ 60
Qy	61	QKLVLYEHYLGTEKLSVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFTQKKPTGS 120
Db	61	QKLVLYEHYLGTEKLSVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFTQKKPTGS 120
Qy	121	IILQOTLTSLVIANFSEPEIKLAQNVITGNSGINLTCTSKQHPKPKMYFLITNSTNEY 180
Db	121	IILQOTLTSLVIANFSEPEIKLAQNVITGNSGINLTCTSKQHPKPKMYFLITNSTNEY 180
Qy	181	GDNMQISQDNVTLEFSLNSLSLSPDGVWHTVVCVLETESMKISSKPLNFTQEPSPQ 240
Db	181	GDNMQISQDNVTLEFSLNSLSLSPDGVWHTVVCVLETESMKISSKPLNFTQEPSPQ 240
Qy	241	TYWKEITASVTALLVLLIIVCHKKPNQPSNTASKLERDSNADRETINLKELEPQ 300

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Db 241 TYWKEITASVTVALLLVLLIIIVCHKKPNQSPSNTASKLERSNADRETINLKELEPQ 300
Qy 301 IASAKPNAE 309
Db 301 IASAKPNAE 309

RESULT 2
US-09-441-411-18
; Sequence 18, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-18

Query Match 100.0%; Score 1599; DB 9; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.7e-119;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPRCTMGLAILIFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSLVVFWQDQ 60
Db 1 MDPRCTMGLAILIFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSLVVFWQDQ 60
Qy 61 QKLVLVEHYLGTGKLDSDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSDYDCFIQKKPPTGS 120
Db 61 QKLVLVEHYLGTGKLDSDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSDYDCFIQKKPPTGS 120
Qy 121 IILQOQLTSLSVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKPKMYFLITNSTNEY 180
Db 121 IILQOQLTSLSVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKPKMYFLITNSTNEY 180
Qy 181 GDNMQISQDNVTLEFSISLSLSPDPGVVHMTVVCVLETESMKISSKPLNFTOEFTSPQ 240
Db 181 GDNMQISQDNVTLEFSISLSLSPDPGVVHMTVVCVLETESMKISSKPLNFTOEFTSPQ 240
Qy 241 TYWKEITASVTVALLLVLLIIIVCHKKPNQSPSNTASKLERSNADRETINLKELEPQ 300
Db 241 TYWKEITASVTVALLLVLLIIIVCHKKPNQSPSNTASKLERSNADRETINLKELEPQ 300
Qy 301 IASAKPNAE 309
Db 301 IASAKPNAE 309

RESULT 3
US-09-441-411-24
; Sequence 24, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-24

Query Match 100.0%; Score 1599; DB 9; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.7e-119;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPRCTMGLAILIFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSLVVFWQDQ 60
Db 1 MDPRCTMGLAILIFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSLVVFWQDQ 60
Qy 61 QKLVLVEHYLGTGKLDSDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSDYDCFIQKKPPTGS 120
Db 61 QKLVLVEHYLGTGKLDSDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSDYDCFIQKKPPTGS 120
Qy 121 IILQOQLTSLSVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKPKMYFLITNSTNEY 180
Db 121 IILQOQLTSLSVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKPKMYFLITNSTNEY 180
Qy 181 GDNMQISQDNVTLEFSISLSLSPDPGVVHMTVVCVLETESMKISSKPLNFTOEFTSPQ 240
Db 181 GDNMQISQDNVTLEFSISLSLSPDPGVVHMTVVCVLETESMKISSKPLNFTOEFTSPQ 240
Qy 241 TYWKEITASVTVALLLVLLIIIVCHKKPNQSPSNTASKLERSNADRETINLKELEPQ 300
Db 241 TYWKEITASVTVALLLVLLIIIVCHKKPNQSPSNTASKLERSNADRETINLKELEPQ 300
Qy 301 IASAKPNAE 309
Db 301 IASAKPNAE 309

RESULT 4
US-09-837-867A-21
; Sequence 21, Application US/09837867A
; Patent No. US20020098542A1
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Bortello, Francescopaulo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. US20020098542A1el Forms of T Cell Costimulatory
; FILE REFERENCE: BWI-120CPADV
; CURRENT APPLICATION NUMBER: US/09/837,867A
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 08/205,697
; PRIOR FILING DATE: 1994-03-02
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-837-867A-21

Query Match 100.0%; Score 1599; DB 10; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.7e-119;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPRCTMGLAILIFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSLVVFWQDQ 60
Db 1 MDPRCTMGLAILIFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSLVVFWQDQ 60
Qy 61 QKLVLVEHYLGTGKLDSDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSDYDCFIQKKPPTGS 120
Db 61 QKLVLVEHYLGTGKLDSDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSDYDCFIQKKPPTGS 120
Qy 121 IILQOQLTSLSVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKPKMYFLITNSTNEY 180
Db 121 IILQOQLTSLSVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKPKMYFLITNSTNEY 180
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; SEQ ID NO 24
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-24

Query Match 100.0%; Score 1599; DB 9; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.7e-119;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPRCTMGLAILIFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSLVVFWQDQ 60
Db 1 MDPRCTMGLAILIFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSLVVFWQDQ 60
Qy 61 QKLVLVEHYLGTGKLDSDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSDYDCFIQKKPPTGS 120
Db 61 QKLVLVEHYLGTGKLDSDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSDYDCFIQKKPPTGS 120
Qy 121 IILQOQLTSLSVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKPKMYFLITNSTNEY 180
Db 121 IILQOQLTSLSVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKPKMYFLITNSTNEY 180
Qy 181 GDNMQISQDNVTLEFSISLSLSPDPGVVHMTVVCVLETESMKISSKPLNFTOEFTSPQ 240
Db 181 GDNMQISQDNVTLEFSISLSLSPDPGVVHMTVVCVLETESMKISSKPLNFTOEFTSPQ 240
Qy 241 TYWKEITASVTVALLLVLLIIIVCHKKPNQSPSNTASKLERSNADRETINLKELEPQ 300
Db 241 TYWKEITASVTVALLLVLLIIIVCHKKPNQSPSNTASKLERSNADRETINLKELEPQ 300
Qy 301 IASAKPNAE 309
Db 301 IASAKPNAE 309

RESULT 4
US-09-837-867A-21
; Sequence 21, Application US/09837867A
; Patent No. US20020098542A1
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Bortello, Francescopaulo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. US20020098542A1el Forms of T Cell Costimulatory
; FILE REFERENCE: BWI-120CPADV
; CURRENT APPLICATION NUMBER: US/09/837,867A
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 08/205,697
; PRIOR FILING DATE: 1994-03-02
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-837-867A-21

Query Match 100.0%; Score 1599; DB 10; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.7e-119;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPRCTMGLAILIFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSLVVFWQDQ 60
Db 1 MDPRCTMGLAILIFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSLVVFWQDQ 60
Qy 61 QKLVLVEHYLGTGKLDSDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSDYDCFIQKKPPTGS 120
Db 61 QKLVLVEHYLGTGKLDSDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSDYDCFIQKKPPTGS 120
Qy 121 IILQOQLTSLSVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKPKMYFLITNSTNEY 180
Db 121 IILQOQLTSLSVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKPKMYFLITNSTNEY 180
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Db 121 ILQQTUTEISVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKKMYFLITNSTNEY 180
QY 181 GDNMQISODNVTELFISINSLSLSPDGVVHMTVVCVLETESMKISSKPLNFTQEPFSPQ 240
Db 181 GDNMQISODNVTELFISINSLSLSPDGVVHMTVVCVLETESMKISSKPLNFTQEPFSPQ 240
QY 241 TWKEITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERSDNADRETINLKELEPQ 300
Db 241 TWKEITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERSDNADRETINLKELEPQ 300
QY 301 IASAKPNAE 309
Db 301 IASAKPNAE 309

RESULT 5
US-09-441-411-14
; Sequence 14, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441.411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-14

Query Match 98.6%; Score 1576; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.8e-117;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CTMGLAILIFVTVLLISDAVSVEIQAYFNGTAYLPCPFTKAQNISLSSELVVFWDQOKLV 64
Db 10 CTMGLAILIFVTVLLISDAVSVEIQAYFNGTAYLPCPFTKAQNISLSSELVVFWDQOKLV 69
QY 65 LYEHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVQIKDMGSDYDCFIQKKPPTGSIILQ 124
Db 70 LYEHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVQIKDMGSDYDCFIQKKPPTGSIILQ 129
QY 125 QTLTELSVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNM 184
Db 130 QTLTELSVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNM 189
QY 185 QISODNVTELFISINSLSLSPDGVVHMTVVCVLETESMKISSKPLNFTQEPFSPQTYWK 244
Db 190 QISODNVTELFISINSLSLSPDGVVHMTVVCVLETESMKISSKPLNFTQEPFSPQTYWK 249
QY 245 EITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERSDNADRETINLKELEPQIASA 304
Db 250 EITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERSDNADRETINLKELEPQIASA 309
QY 305 KPNAE 309
Db 310 KPNAE 314

RESULT 6
US-09-441-411-19
; Sequence 19, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd

; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441.411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-19

Query Match 98.6%; Score 1576; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.8e-117;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CTMGLAILIFVTVLLISDAVSVEIQAYFNGTAYLPCPFTKAQNISLSSELVVFWDQOKLV 64
Db 10 CTMGLAILIFVTVLLISDAVSVEIQAYFNGTAYLPCPFTKAQNISLSSELVVFWDQOKLV 69
QY 65 LYEHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVQIKDMGSDYDCFIQKKPPTGSIILQ 124
Db 70 LYEHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVQIKDMGSDYDCFIQKKPPTGSIILQ 129
QY 125 QTLTELSVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNM 184
Db 130 QTLTELSVIANFSEPEIKLAQNVGTGSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNM 189
QY 185 QISODNVTELFISINSLSLSPDGVVHMTVVCVLETESMKISSKPLNFTQEPFSPQTYWK 244
Db 190 QISODNVTELFISINSLSLSPDGVVHMTVVCVLETESMKISSKPLNFTQEPFSPQTYWK 249
QY 245 EITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERSDNADRETINLKELEPQIASA 304
Db 250 EITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERSDNADRETINLKELEPQIASA 309
QY 305 KPNAE 309
Db 310 KPNAE 314

RESULT 7
US-09-837-867A-13
; Sequence 13, Application US/09837867A
; Patent No. US20020098542A1
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Borriello, Francescopaulo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. US20020098542A1el Forms of T Cell Costimulatory
; FILE REFERENCE: BMI-120CPADV
; CURRENT APPLICATION NUMBER: US/09/837.867A
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 08/205,697
; PRIOR FILING DATE: 1994-03-02
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-837-867A-13

Query Match 98.6%; Score 1576; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.8e-117;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CTMGLAILIFVTVLLISDAVSVEIQAYFNGTAYLPCPFTKAQNISLSSELVVFWDQOKLV 64
Db 10 CTMGLAILIFVTVLLISDAVSVEIQAYFNGTAYLPCPFTKAQNISLSSELVVFWDQOKLV 69

Qy	65	LYEHLGTEKLD	SVNAKYLGR	TSDRNNTLRLHN	VQIKDMGSYDCFIQKPP	TGSIILQ	124
Db	70	LYEHLGTEKLD	SVNAKYLGR	TSDRNNTLRLHN	VQIKDMGSYDCFIQKPP	TGSIILQ	129
Qy	125	QTLTELSVIAN	FSPEIKLAQNV	TGNSGINLTCTSK	QGHKPKKMYFLITNST	NEYGDNM	184
Db	130	QTLTELSVIAN	FSPEIKLAQNV	TGNSGINLTCTSK	QGHKPKKMYFLITNST	NEYGDNM	189
Qy	185	QISQDNVTELF	SINSLSLS	FPDGVVHMTVV	CVLETESMKISSKPLN	TQEPFSPQTYWK	244
Db	190	QISQDNVTELF	SINSLSLS	FPDGVVHMTVV	CVLETESMKISSKPLN	TQEPFSPQTYWK	249
Qy	245	EITASVTVAL	LLVMLLI	IVCHKKPNQPS	NTASKLERSNADRET	INLKELEPQIASA	304
Db	250	EITASVTVAL	LLVMLLI	IVCHKKPNQPS	NTASKLERSNADRET	INLKELEPQIASA	309
Qy	305	KPNAE	309				
Db	310	KPNAE	314				
RESULT 8							
US-09-441-411-11							
; Sequence 11, Application US/09441411							
; Publication No. US20030008342A1							
; GENERAL INFORMATION:							
; APPLICANT: Scholler, Nathalie B.							
; APPLICANT: Disis, Mary L.							
; APPLICANT: Hellstrom, Ingegerd							
; APPLICANT: Hellstrom, Karl Erik							
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES							
; FILE REFERENCE: 730033.409							
; CURRENT APPLICATION NUMBER: US/09/441.411							
; CURRENT FILING DATE: 1999-11-16							
; NUMBER OF SEQ ID NOS: 26							
; SOFTWARE: FastSeq for Windows Version 4.0							
; SEQ ID NO 11							
; LENGTH: 356							
; TYPE: PRT							
; ORGANISM: Mus musculus							
US-09-441-411-11							
Query Match 98.0%; Score 1567; DB 9: Length 356;							
Best Local Similarity 100.0%; Pred. No 2,3e-116;							
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Qy	6	TMGAILIFVT	VLLISDAV	SVETQAYFNGTAYL	PCPPTKAQNISISEL	VVFWDQOQKLVL	65
Db	53	TMGAILIFVT	VLLISDAV	SVETQAYFNGTAYL	PCPPTKAQNISISEL	VVFWDQOQKLVL	112
Qy	66	YEHYLGTEKLD	SVNAKYLGR	TSDRNNTLRLHN	VQIKDMGSYDCFIQKPP	TGSIILQ	125
Db	113	YEHYLGTEKLD	SVNAKYLGR	TSDRNNTLRLHN	VQIKDMGSYDCFIQKPP	TGSIILQ	172
Qy	126	TLTLSVIAN	FSPEIKLAQNV	TGNSGINLTCTSK	QGHKPKKMYFLITNST	NEYGDNM	185
Db	173	TLTLSVIAN	FSPEIKLAQNV	TGNSGINLTCTSK	QGHKPKKMYFLITNST	NEYGDNM	232
Qy	186	ISQDNVTELF	SINSLSLS	FPDGVVHMTVV	CVLETESMKISSKPLN	TQEPFSPQTYWK	245
Db	233	ISQDNVTELF	SINSLSLS	FPDGVVHMTVV	CVLETESMKISSKPLN	TQEPFSPQTYWK	292
Qy	246	ITASVTVAL	LLVMLLI	IVCHKKPNQPS	NTASKLERSNADRET	INLKELEPQIASA	305
Db	293	ITASVTVAL	LLVMLLI	IVCHKKPNQPS	NTASKLERSNADRET	INLKELEPQIASA	352
Qy	306	PNAE	309				
Db	353	PNAE	356				

```

US-09-441-411-12
; Sequence 12, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-12

Query Match          98.0%; Score 1567; DB 9; Length 356;
Best Local Similarity 100.0%; Pred. No. 2.3e-116;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6  TWGLAIIFFVTLLISDAVSVEQAYFNGTAYLPCPFTKQAQNISLSLVVFWQDQKQLVL 65
      |||
Db      53  TWGLAIIFFVTLLISDAVSVEQAYFNGTAYLPCPFTKQAQNISLSLVVFWQDQKQLVL 112
      |||

Qy      66  YEHYLGTEKLDVSNAKYLGRTSFDRNNWTLRLHNVOIKDMSYDCFIQKKPPTGSILOQ 125
      |||
Db      113 YEHYLGTEKLDVSNAKYLGRTSFDRNNWTLRLHNVOIKDMSYDCFIQKKPPTGSILOQ 172
      |||

Qy      126  TLTLSLVIANFSPPEIKLAQNVGTSGNINLTCTSKOGHPKPKMYFLITNSTNEYGDNQ 185
      |||
Db      173  TLTLSLVIANFSPPEIKLAQNVGTSGNINLTCTSKOGHPKPKMYFLITNSTNEYGDNQ 232
      |||

Qy      186  ISQDNVTLEFSINSLISLFFPDGVVHMTVCVLETSMKISSKPLNFTQFPFPSPQTYWKE 245
      |||
Db      233  ISQDNVTLEFSINSLISLFFPDGVVHMTVCVLETSMKISSKPLNFTQFPFPSPQTYWKE 292
      |||

Qy      246  ITASVTVALLLVMLLIIVCHKKPNOPSPNTASKLERSDNADRETINLKELEPQIASAK 305
      |||
Db      293  ITASVTVALLLVMLLIIVCHKKPNOPSPNTASKLERSDNADRETINLKELEPQIASAK 352
      |||

Qy      306  PNAE 309
      |||
Db      353  PNAE 356

RESULT 10
US-09-441-411-16
; Sequence 16, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-16

Query Match          98.0%; Score 1567; DB 9; Length 356;
Best Local Similarity 100.0%; Pred. No. 2.3e-116;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
QY 6 TMGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSSELVFWQDOOKLVL 65
Db 53 TMGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSSELVFWQDOOKLVL 112
QY 66 YHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMSYDCFIQKKPPTGSIILQQ 125
Db 113 YHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMSYDCFIQKKPPTGSIILQQ 172
QY 126 TLTELSVIANFSEPEIKLAQNTGNSGINTCTSKQGHKPKKMYFLITNSTNEYGDNMQ 185
Db 173 TLTELSVIANFSEPEIKLAQNTGNSGINTCTSKQGHKPKKMYFLITNSTNEYGDNMQ 232
QY 186 ISQDNVTELSFNSLSLSPFDGWHMTVVCVLETESMKISSKPLNFTOEFPSPQTYWKE 245
Db 233 ISQDNVTELSFNSLSLSPFDGWHMTVVCVLETESMKISSKPLNFTOEFPSPQTYWKE 292
QY 246 ITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPOIASAK 305
Db 293 ITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPOIASAK 352
QY 306 PNAE 309
Db 353 PNAE 356

RESULT 11
US-09-441-411-17
; Sequence 17, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441.411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-17

Query Match 98.0%; Score 1567; DB 9; Length 356;
Best Local Similarity 100.0%; Pred. No. 2.3e-116;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TMGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSSELVFWQDOOKLVL 65
Db 53 TMGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSSELVFWQDOOKLVL 112
QY 66 YHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMSYDCFIQKKPPTGSIILQQ 125
Db 113 YHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMSYDCFIQKKPPTGSIILQQ 172
QY 126 TLTELSVIANFSEPEIKLAQNTGNSGINTCTSKQGHKPKKMYFLITNSTNEYGDNMQ 185
Db 173 TLTELSVIANFSEPEIKLAQNTGNSGINTCTSKQGHKPKKMYFLITNSTNEYGDNMQ 232
QY 186 ISQDNVTELSFNSLSLSPFDGWHMTVVCVLETESMKISSKPLNFTOEFPSPQTYWKE 245
Db 233 ISQDNVTELSFNSLSLSPFDGWHMTVVCVLETESMKISSKPLNFTOEFPSPQTYWKE 292
QY 246 ITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPOIASAK 305
Db 293 ITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPOIASAK 352
QY 306 PNAE 309
Db 353 PNAE 356

RESULT 12
US-09-441-411-15
; Sequence 15, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441.411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-15

Query Match 97.7%; Score 1562; DB 9; Length 303;
Best Local Similarity 100.0%; Pred. No. 4.6e-116;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSSELVFWQDOOKLVL 66
Db 1 MGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSSELVFWQDOOKLVL 60
QY 67 EHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMSYDCFIQKKPPTGSIILQQ 126
Db 61 EHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMSYDCFIQKKPPTGSIILQQ 120
QY 127 LTSELSVIANFSEPEIKLAQNTGNSGINTCTSKQGHKPKKMYFLITNSTNEYGDNMQ 186
Db 121 LTSELSVIANFSEPEIKLAQNTGNSGINTCTSKQGHKPKKMYFLITNSTNEYGDNMQ 180
QY 187 SQDNVTELSFNSLSLSPFDGWHMTVVCVLETESMKISSKPLNFTOEFPSPQTYWKEI 246
Db 181 SQDNVTELSFNSLSLSPFDGWHMTVVCVLETESMKISSKPLNFTOEFPSPQTYWKEI 240
QY 247 TASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPOIASAK 306
Db 241 TASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPOIASAK 300
QY 307 NAE 309
Db 301 NAE 303

RESULT 13
US-09-441-411-20
; Sequence 20, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441.411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-20
```

```
Db 353 PNAE 356

RESULT 12
US-09-441-411-15
; Sequence 15, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441.411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-15

Query Match 97.7%; Score 1562; DB 9; Length 303;
Best Local Similarity 100.0%; Pred. No. 4.6e-116;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSSELVFWQDOOKLVL 66
Db 1 MGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPPTKAQNISLSSELVFWQDOOKLVL 60
QY 67 EHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMSYDCFIQKKPPTGSIILQQ 126
Db 61 EHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMSYDCFIQKKPPTGSIILQQ 120
QY 127 LTSELSVIANFSEPEIKLAQNTGNSGINTCTSKQGHKPKKMYFLITNSTNEYGDNMQ 186
Db 121 LTSELSVIANFSEPEIKLAQNTGNSGINTCTSKQGHKPKKMYFLITNSTNEYGDNMQ 180
QY 187 SQDNVTELSFNSLSLSPFDGWHMTVVCVLETESMKISSKPLNFTOEFPSPQTYWKEI 246
Db 181 SQDNVTELSFNSLSLSPFDGWHMTVVCVLETESMKISSKPLNFTOEFPSPQTYWKEI 240
QY 247 TASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPOIASAK 306
Db 241 TASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPOIASAK 300
QY 307 NAE 309
Db 301 NAE 303

RESULT 13
US-09-441-411-20
; Sequence 20, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441.411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-20
```

```
Query Match          97.7%; Score 1562; DB 9; Length 303;
Best Local Similarity 100.0%; Pred. No. 4.6e-116; Indels 0; Gaps 0;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGLAIFVTVLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLVVFWDDQKLVLV 66
   |||||
Db 1 MGLAIFVTVLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLVVFWDDQKLVLV 60

QY 67 EHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGSIILQOT 126
   |||||
Db 61 EHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGSIILQOT 120

QY 127 LTLSLVIANFSEPEIKLAQNVGTSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNNQI 186
   |||||
Db 121 LTLSLVIANFSEPEIKLAQNVGTSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNNQI 180

QY 187 SODNVTELSISLSLSPDGVHMTVVCVLETESMKISSKPLNFTQEFPSPTYWKEI 246
   |||||
Db 181 SODNVTELSISLSLSPDGVHMTVVCVLETESMKISSKPLNFTQEFPSPTYWKEI 240

QY 247 TASVTVALLVMLLIIVCHVCKENQPSRPSNTASKLERDSNADRETINLKELEPOIASAKP 306
   |||||
Db 241 TASVTVALLVMLLIIVCHVCKENQPSRPSNTASKLERDSNADRETINLKELEPOIASAKP 300

QY 307 NAE 309
   ||||
Db 301 NAE 303

RESULT 14
US-08-592-711-4
; Sequence 4; Application US/08592711
; Patent No. US20020115214A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennett, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,711
; FILING DATE: 26-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,816
; FILING DATE: 4-MAY-1995
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: 10-MARCH-1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3-JUNE-1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4-JUNE-1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23-FEB-1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 07/864,866
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; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25-MAR-1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16-JUNE-1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-592-711-4

Query Match          46.5%; Score 743.5; DB 8; Length 329;
Best Local Similarity 51.5%; Pred. No. 1.8e-51;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

QY 1 MDPRCTMGLAIFVTVLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLVVFWDDQ 60
   |||||
Db 1 MDPCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSQNSLSLVVFWDDQ 60

QY 61 OKLVLYEHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGS 120
   |||||
Db 61 ENLVLYEVLYGCKEFDVSHVSKYWGRTSFDSDSWTLRLHNLOIKDKGLYQCIIHHKKPTGM 120

QY 121 ILQOQTLTELSLVIANFSEPEIKLAQNVGTSGINLTCTSKQGHKPKKMYFLI--TNSTN 178
   |||||
Db 121 IRIHQMSLSLVIANFSEPEIVPISNITENVYINLTCSHGYPEPKKMSVLLRTKNSTI 180

QY 179 EYGDNMOISODNVTELSISLSLSPDGVHMTVVCVLETESMKISSKPLNFTQEFPS 238
   |||||
Db 181 EYDGMQKSQDNVTLYDVSLSVSFFDVTNSNWTIFCILETDKTRLLSSPFSIELEDPQ 240

QY 239 P---QTYWKEITASVTVALLVLM--LIIVCHVCKENQPSRP----SNTASKLERDSNADR 289
   |||||
Db 241 PPPDHIPW--ITAVLPTVTCVWFCLILWKWKKKRPRNSYKCGTNTMREESQTKKR 298

QY 290 ETINLKE 296
   ||||
Db 299 EXHIPE 305

RESULT 15
US-09-441-411-26
; Sequence 26; Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-441-411-26
```

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Query Match      46.5%; Score 743.5; DB 9; Length 329;
Best Local Similarity 51.5%; Pred No. 1.8e-51;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

Qy 1 MDPRTMGUAIIFVTVLLISDAVSVEIQAYFNGTAYLPCPTKAQNISLSLVVFWQDQ 60
Db 1 MDPQCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSLVVFWQDQ 60

Qy 61 QKLVLYEHYLGTEKLDVNAKYLGRTSFDNRNNTLRHNVQIKDMGSYDCFIQKKPPTGS 120
Db 61 ENLVLEVYLGKEKEDSVHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIHHKKPTGM 120

Qy 121 IILQQLTELTVIANFSPEIKLAQNVGTGNSGINLTCTSKQGHKPKKMYFLI--TNSTN 178
Db 121 IRIHQMNSELVLANFSQPEIVPISNITENVYINLTCSIHGYPEPKMSVLLRTKNSTI 180

Qy 179 EYGDNMQISQDNVTLEFSISNLSLSPDPGVHMTVVCVLETESMKISSKPLNFTQEPFS 238
Db 181 EYDGIQKQSDNVTELYDVSISLSPDPVTSNWTIFCILETDKTRLLSSPFSIELEDPO 240

Qy 239 P---QTYWKEITASVTVALLLVML--LIIVCHKKPNQPSRP----SNTASKLERDSNADR 289
Db 241 PPPDHIPW--ITAVLPTVILCVMVFCILMKWKKKKRPRNSYKCGTNTMERESEQTKKR 298

Qy 290 ETINLKE 296
Db 299 EKIHIPE 305

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Search completed: February 13, 2003, 11:39:58
Job time : 17.9514 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 11:29:49 ; Search time 12.1082 Seconds
(without alignments)
750.873 Million cell updates/sec

Title: US-09-425-516-23

Perfect score: 1599

Sequence: 1 MDRPCTMGLAIFVTLLI.....ETINLKEPQIASAKPNAE 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents:AA*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
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5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1599	100.0	309	2	US-08-456-104-4
2	1599	100.0	309	3	US-08-479-744A-23
3	1599	100.0	309	4	US-08-280-757B-23
4	1599	100.0	309	4	US-08-205-697A-21
5	1599	100.0	309	4	US-08-702-525-21
6	1599	100.0	309	4	US-09-651-200-22
7	1599	100.0	309	5	PCT-US95-02576-21
8	1576	98.6	314	4	US-08-205-697A-13
9	1576	98.6	314	4	US-08-702-525-13
10	1576	98.6	314	5	PCT-US95-02576-13
11	1562	97.7	303	4	US-09-651-200-23
12	743.5	46.5	329	2	US-08-456-104-2
13	743.5	46.5	329	2	US-08-101-624-2
14	743.5	46.5	329	3	US-08-479-744A-2
15	743.5	46.5	329	4	US-08-280-757B-2
16	743.5	46.5	329	4	US-08-205-697A-23
17	743.5	46.5	329	4	US-08-702-525-23
18	743.5	46.5	329	4	US-08-403-253A-4
19	743.5	46.5	329	5	PCT-US95-02576-23
20	710.5	44.4	323	4	US-09-651-200-21
21	710.5	44.4	323	5	PCT-US94-09642-2
22	694	43.4	329	4	US-09-651-200-19
23	662	41.4	325	4	US-09-651-200-20
24	640.5	40.1	329	4	US-09-651-200-18
25	508	31.8	95	4	US-08-928-383B-10
26	358	22.4	110	3	US-08-479-744A-45
27	358	22.4	110	4	US-08-280-757B-45

28	260	16.3	102	3	US-08-479-744A-47	Sequence 47, Appl
29	260	16.3	102	4	US-08-280-757B-47	Sequence 47, Appl
30	230	14.4	45	4	US-08-205-697A-30	Sequence 30, Appl
31	230	14.4	45	4	US-08-702-525-30	Sequence 30, Appl
32	230	14.4	45	5	PCT-US95-02576-30	Sequence 30, Appl
33	227.5	14.2	306	4	US-08-205-697A-17	Sequence 17, Appl
34	227.5	14.2	306	4	US-08-702-525-17	Sequence 17, Appl
35	227.5	14.2	306	4	US-09-651-200-17	Sequence 17, Appl
36	227.5	14.2	306	5	PCT-US95-02576-17	Sequence 17, Appl
37	226.5	14.2	306	2	US-08-147-772-4	Sequence 4, Appl
38	226.5	14.2	306	2	US-08-456-104-8	Sequence 8, Appl
39	226.5	14.2	306	2	US-08-101-624-25	Sequence 25, Appl
40	226.5	14.2	306	3	US-08-153-262-4	Sequence 4, Appl
41	226.5	14.2	306	3	US-08-479-744A-31	Sequence 31, Appl
42	226.5	14.2	306	4	US-08-280-757B-31	Sequence 31, Appl
43	226.5	14.2	306	4	US-09-159-135-4	Sequence 4, Appl
44	226.5	14.2	306	4	US-09-450-798-4	Sequence 4, Appl
45	212	13.3	320	4	US-08-205-697A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-456-104-4
; Sequence 4, Application US/08456104
; Patent No. 5861310
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,104
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624;
; FILING DATE: 26-JUL-1993;
; APPLICATION NUMBER: 08/109,393;
; APPLICATION NUMBER: 19-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoutas, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-456-104-4

Query Match 100.0%; Score 1599; DB 2; Length 309;
Best Local Similarity 100.0%; Pred. No. 3.2e-139;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPRTMGLAIIIFVTVLLISDAVSVEQAVFNGTAYLPCPFTKAQNTLSLSLVFWQDQ 60
Db 1 MDPRTMGLAIIIFVTVLLISDAVSVEQAVFNGTAYLPCPFTKAQNTLSLSLVFWQDQ 60
QY 61 QKLVLYEHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVQIKDMGSYDCFTQKKPPTGS 120
Db 61 QKLVLYEHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVQIKDMGSYDCFTQKKPPTGS 120
QY 121 ILLOQTLETLSVIANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKPKMYFLITNSTNEY 180
Db 121 ILLOQTLETLSVIANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKPKMYFLITNSTNEY 180
QY 181 GDNMQISQDNVTELFISNSLSLSPFDGWHMTVVCVLETESMKISSKPLNFTQBFPSQ 240
Db 181 GDNMQISQDNVTELFISNSLSLSPFDGWHMTVVCVLETESMKISSKPLNFTQBFPSQ 240
QY 241 TYWKEITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQ 300
Db 241 TYWKEITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQ 300
QY 301 IASAKPNAE 309
Db 301 IASAKPNAE 309
RESULT 2
US-08-479-744A-23
; Sequence 23, Application US/08479744A
; Patent No. 6084067
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses therefor
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,744A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/280,757
; FILING DATE: 26-JUL-1994
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 28-AUG-1993
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-479-744A-23
Query Match 100.0%; Score 1599; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. NO. 3.2e-139;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDPRTMGLAIIIFVTVLLISDAVSVEQAVFNGTAYLPCPFTKAQNTLSLSLVFWQDQ 60
Db 1 MDPRTMGLAIIIFVTVLLISDAVSVEQAVFNGTAYLPCPFTKAQNTLSLSLVFWQDQ 60
QY 61 QKLVLYEHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVQIKDMGSYDCFTQKKPPTGS 120
Db 61 QKLVLYEHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVQIKDMGSYDCFTQKKPPTGS 120
QY 121 ILLOQTLETLSVIANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKPKMYFLITNSTNEY 180
Db 121 ILLOQTLETLSVIANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKPKMYFLITNSTNEY 180
QY 181 GDNMQISQDNVTELFISNSLSLSPFDGWHMTVVCVLETESMKISSKPLNFTQBFPSQ 240
Db 181 GDNMQISQDNVTELFISNSLSLSPFDGWHMTVVCVLETESMKISSKPLNFTQBFPSQ 240
QY 241 TYWKEITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQ 300
Db 241 TYWKEITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQ 300
QY 301 IASAKPNAE 309
Db 301 IASAKPNAE 309
RESULT 3
US-08-280-757B-23
; Sequence 23, Application US/08280757B
; Patent No. 6130316
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; APPLICANT: Greenfield, Edward
; TITLE OF INVENTION: No. 6130316el CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/280,757B
; FILING DATE: 26-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-280-757B-23

Query Match 100.0%; Score 1599; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 3.2e-139;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDPRTMGALILIFVTLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSSELVFWQDQ 60
DB 1 MDPRTMGALILIFVTLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSSELVFWQDQ 60
QY 61 QKLVLVEHYLGTGKLDVNAKYLGRISFDRNNWTLRLHNVOIKDMGSYDCFIQKPPPTGS 120
DB 61 QKLVLVEHYLGTGKLDVNAKYLGRISFDRNNWTLRLHNVOIKDMGSYDCFIQKPPPTGS 120
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DB 121 ILQOTLTLSLVIANFSEPEIKLAQNVTONSGINLTCTSKQGHKPKKMYFLITNSTNEY 180
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DB 181 GDNMQISQDNVTLEFSISNSLSLSPDGVVHMTVVCVLETESMKISSKPLNFTQEPSPQ 240
QY 241 TYWKEITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQ 300
DB 241 TYWKEITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQ 300
QY 301 IASAKPNAE 309
DB 301 IASAKPNAE 309

RESULT 4

US-08-205-697A-21
Sequence 21, Application US/08205697A
Patent No. 6218510
GENERAL INFORMATION:
APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/205,697A
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-205-697A-21

Query Match 100.0%; Score 1599; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 3.2e-139;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDPRTMGALILIFVTLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSSELVFWQDQ 60
DB 1 MDPRTMGALILIFVTLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSSELVFWQDQ 60
QY 61 QKLVLVEHYLGTGKLDVNAKYLGRISFDRNNWTLRLHNVOIKDMGSYDCFIQKPPPTGS 120
DB 61 QKLVLVEHYLGTGKLDVNAKYLGRISFDRNNWTLRLHNVOIKDMGSYDCFIQKPPPTGS 120
QY 121 ILQOTLTLSLVIANFSEPEIKLAQNVTONSGINLTCTSKQGHKPKKMYFLITNSTNEY 180
DB 121 ILQOTLTLSLVIANFSEPEIKLAQNVTONSGINLTCTSKQGHKPKKMYFLITNSTNEY 180
QY 181 GDNMQISQDNVTLEFSISNSLSLSPDGVVHMTVVCVLETESMKISSKPLNFTQEPSPQ 240
DB 181 GDNMQISQDNVTLEFSISNSLSLSPDGVVHMTVVCVLETESMKISSKPLNFTQEPSPQ 240
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DB 241 TYWKEITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQ 300
QY 301 IASAKPNAE 309
DB 301 IASAKPNAE 309

RESULT 5

US-08-702-525-21
Sequence 21, Application US/08702525
Patent No. 6294660
GENERAL INFORMATION:
APPLICANT: Sharpe, Sharpe
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Gordon
APPLICANT: Nadler, Lee
TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory Molecules and Uses Therefor
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,525
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120CPUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-702-525-21

Query Match 100.0%; Score 1599; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 3.2e-139;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPRCTMGLAILFVTVLLISDAVSVEYQAYFNGTAYLPCPFTKAQNISLSLVVFWDDQ 60
DB 1 MDPRCTMGLAILFVTVLLISDAVSVEYQAYFNGTAYLPCPFTKAQNISLSLVVFWDDQ 60

QY 61 OKLVLYEHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGS 120
DB 61 OKLVLYEHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGS 120

QY 121 IILQOTLTLSVIANFSEPEIKLAQNVGTGNSGINTCTSKQGHKPKKMYFLITNSTNEY 180
DB 121 IILQOTLTLSVIANFSEPEIKLAQNVGTGNSGINTCTSKQGHKPKKMYFLITNSTNEY 180

QY 181 GDNMOISQDNVTELFISNSLSLSPDGVVHMTVVVCLTESMKISSKPLNFTQEPFSPQ 240
DB 181 GDNMOISQDNVTELFISNSLSLSPDGVVHMTVVVCLTESMKISSKPLNFTQEPFSPQ 240

QY 241 TWKKEITASVTVALLLVMLLIIVCHKKNPQSRPSNTASKLERSNADRETINLKELEPQ 300
DB 241 TWKKEITASVTVALLLVMLLIIVCHKKNPQSRPSNTASKLERSNADRETINLKELEPQ 300

QY 301 IASAKPNAE 309
DB 301 IASAKPNAE 309

RESULT 6

US-09-651-200-22
; Sequence 22, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651.200
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-651-200-22

Query Match 100.0%; Score 1599; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 3.2e-139;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPRCTMGLAILFVTVLLISDAVSVEYQAYFNGTAYLPCPFTKAQNISLSLVVFWDDQ 60
DB 1 MDPRCTMGLAILFVTVLLISDAVSVEYQAYFNGTAYLPCPFTKAQNISLSLVVFWDDQ 60

QY 61 OKLVLYEHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGS 120
DB 61 OKLVLYEHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGS 120

DB 61 OKLVLYEHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGS 120
QY 121 IILQOTLTLSVIANFSEPEIKLAQNVGTGNSGINTCTSKQGHKPKKMYFLITNSTNEY 180
DB 121 IILQOTLTLSVIANFSEPEIKLAQNVGTGNSGINTCTSKQGHKPKKMYFLITNSTNEY 180
QY 181 GDNMOISQDNVTELFISNSLSLSPDGVVHMTVVVCLTESMKISSKPLNFTQEPFSPQ 240
DB 181 GDNMOISQDNVTELFISNSLSLSPDGVVHMTVVVCLTESMKISSKPLNFTQEPFSPQ 240
QY 241 TWKKEITASVTVALLLVMLLIIVCHKKNPQSRPSNTASKLERSNADRETINLKELEPQ 300
DB 241 TWKKEITASVTVALLLVMLLIIVCHKKNPQSRPSNTASKLERSNADRETINLKELEPQ 300
QY 301 IASAKPNAE 309
DB 301 IASAKPNAE 309

RESULT 7

PCT-US95-02576-21
; Sequence 21, Application PC/TUS9502576
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
; TITLE OF INVENTION: and Uses Therefor
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02576
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy B.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120CPPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-02576-21

Query Match 100.0%; Score 1599; DB 5; Length 309;
Best Local Similarity 100.0%; Pred. No. 3.2e-139;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPRCTMGLAILFVTVLLISDAVSVEYQAYFNGTAYLPCPFTKAQNISLSLVVFWDDQ 60
DB 1 MDPRCTMGLAILFVTVLLISDAVSVEYQAYFNGTAYLPCPFTKAQNISLSLVVFWDDQ 60

QY 61 OKLVLYEHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGS 120
DB 61 OKLVLYEHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGS 120
QY 121 IILQOTLTLSVIANFSEPEIKLAQNVGTGNSGINTCTSKQGHKPKKMYFLITNSTNEY 180

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Db 121 IILQOTLTVSIVANFSEPIKLAQNVGTGNSGINLTCTSKQGHKPKMYFLITNSTNEY 180
QY 181 GDMQISODNVTELSFISNSLSLSPDGVHMTVVCVLETESMKISSKPLNFTQEFPSQTYWK 240
Db 181 GDMQISODNVTELSFISNSLSLSPDGVHMTVVCVLETESMKISSKPLNFTQEFPSQTYWK 240
QY 241 TYWKITASVTVALLLVLLIIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQIASA 304
Db 241 TYWKITASVTVALLLVLLIIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQIASA 309
QY 301 IASAKPNAE 309
Db 301 IASAKPNAE 309

RESULT 8
US-08-205-697A-13
; Sequence 13, Application US/08205697A
; Patent No. 6218510
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Borriello, Francescopaolo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
; and Uses Therefor
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/205,697A
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-205-697A-13

Query Match 98.6%; Score 1576; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTMGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLVVFWQDOQKLV 64
Db 10 CTMGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLVVFWQDOQKLV 69
QY 65 LYEHVLGTEKLDVSNAYKLGRTSFRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGSIILQ 124
Db 70 LYEHVLGTEKLDVSNAYKLGRTSFRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGSIILQ 129
QY 125 QTLTSLVIANFSEPIKLAQNVGTGNSGINLTCTSKQGHKPKMYFLITNSTNEYGDNM 184
Db 130 QTLTSLVIANFSEPIKLAQNVGTGNSGINLTCTSKQGHKPKMYFLITNSTNEYGDNM 189
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QY 185 QISODNVTELSISNSLSLSPDGVHMTVVCVLETESMKISSKPLNFTQEFPSQTYWK 244
Db 190 QISODNVTELSISNSLSLSPDGVHMTVVCVLETESMKISSKPLNFTQEFPSQTYWK 249
QY 245 EITASVTVALLLVLLIIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQIASA 304
Db 250 EITASVTVALLLVLLIIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQIASA 309
QY 305 KPNAE 309
Db 310 KPNAE 314

RESULT 9
US-08-702-525-13
; Sequence 13, Application US/08702525
; Patent No. 6294660
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Sharpe
; APPLICANT: Borriello, Francescopaolo
; APPLICANT: Freeman, Gordon
; APPLICANT: Nadler, Lee
; TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory
; Molecules and Uses Therefor
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,525
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120CPUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-702-525-13

Query Match 98.6%; Score 1576; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTMGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLVVFWQDOQKLV 64
Db 10 CTMGLAILFVTVLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLVVFWQDOQKLV 69
QY 65 LYEHVLGTEKLDVSNAYKLGRTSFRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGSIILQ 124
Db 70 LYEHVLGTEKLDVSNAYKLGRTSFRNNWTLRLHNVOIKDMGSYDCFIQKKPPTGSIILQ 129
QY 125 QTLTSLVIANFSEPIKLAQNVGTGNSGINLTCTSKQGHKPKMYFLITNSTNEYGDNM 184
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Db 130 QTLTSLSVIANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNM 189
QY 185 QISQDNVTFLFSISNSLSLSPFDGVVHMTVVCVLETESMKISSKPLNFTQEPFSPQTYWK 244
Db 190 QISQDNVTFLFSISNSLSLSPFDGVVHMTVVCVLETESMKISSKPLNFTQEPFSPQTYWK 249
QY 245 EITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQIASA 304
Db 250 EITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQIASA 309
QY 305 KPNAE 309
Db 310 KPNAE 314

RESULT 10
PCT-US95-02576-13
; Sequence 13, Application PC/TUS9502576
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02576
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120CPCC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-02576-13

Query Match 98.6%; Score 1576; DB 5; Length 314;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTMGLAILIFVTVLLISDAVSVEVQAYFNGTAYLPCPFTKAQNISLSLWVFWQDQOKLV 64
Db 10 CTMGLAILIFVTVLLISDAVSVEVQAYFNGTAYLPCPFTKAQNISLSLWVFWQDQOKLV 69
QY 65 LYEHVLGTEKLDVSNAYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPTGSIILQ 124
Db 70 LYEHVLGTEKLDVSNAYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPTGSIILQ 129
QY 125 QTLTSLSVIANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNM 184
Db 130 QTLTSLSVIANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNM 189
QY 185 QISQDNVTFLFSISNSLSLSPFDGVVHMTVVCVLETESMKISSKPLNFTQEPFSPQTYWK 244

Db 190 QISQDNVTFLFSISNSLSLSPFDGVVHMTVVCVLETESMKISSKPLNFTQEPFSPQTYWK 249
QY 245 EITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQIASA 304
Db 250 EITASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQIASA 309
QY 305 KPNAE 309
Db 310 KPNAE 314

RESULT 11
US-09-651-200-23
; Sequence 23, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651,200
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-651-200-23

Query Match 97.7%; Score 1562; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 8e-136;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGLAILIFVTVLLISDAVSVEVQAYFNGTAYLPCPFTKAQNISLSLWVFWQDQOKLV 66
Db 1 MGLAILIFVTVLLISDAVSVEVQAYFNGTAYLPCPFTKAQNISLSLWVFWQDQOKLV 60
QY 67 EHYLGTEDKLDVSNAYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPTGSIILQ 126
Db 61 EHYLGTEDKLDVSNAYLGRTSFDRNNWTLRLHNVOIKDMGSYDCFIQKKPTGSIILQ 120
QY 127 LTLSLVIANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNM 186
Db 121 LTLSLVIANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKKMYFLITNSTNEYGDNM 180
QY 187 SQDNVTFLFSISNSLSLSPFDGVVHMTVVCVLETESMKISSKPLNFTQEPFSPQTYWK 246
Db 181 SQDNVTFLFSISNSLSLSPFDGVVHMTVVCVLETESMKISSKPLNFTQEPFSPQTYWK 240
QY 247 TASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQIASAKP 306
Db 241 TASVTVALLLVMLLIIVCHKKPNQPSRPSNTASKLERDSNADRETINLKELEPQIASAKP 300
QY 307 NAE 309
Db 301 NAE 303

RESULT 12
US-08-456-104-2
; Sequence 2, Application US/08456104
; Patent No. 5861310
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.

APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,104
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-456-104-2

Query Match 46.5%; Score 743.5; DB 2; Length 329;
Best Local Similarity 51.5%; Pred. No. 1.7e-60;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;
QY 1 MDPRTCTMGLAIIIFVTYLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLVFWQDQ 60
Db 1 MDPQCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSONQSLSELVFWQDQ 60
QY 61 OKLVLYEHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNQIKDMSYDCFIQKKPPTGS 120
Db 61 ENLVNEVYLGEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGM 120
QY 121 ILQOQLTSLSVIANFSEPEIKLAQNVGTGNSGINLTCTSKQHPKPKMYFLI--TNSTN 178
Db 121 IRIHQMSLSVLANSFQPEIPIVSNITENVYINLTCSIHGYEPKPKMSVLLRTKNSI 180
QY 179 EYGNMIOSONVTELSISLSLSPDGVMHVTVCVLETSKMKISSKPLNFTQFPFS 238
Db 181 EYDGMQSQDNVTELYDVSISLSVFPDVTNSMTIFCILETDKTLRLSSPFIIEPDQ 240
QY 239 P---QTYWKEITASVTVALLLVNL--LIIVCHKPKNPQSRP-----SNTASKLERSNADR 289
Db 241 PPPDHIPW--ITAVLPVVICVWFCLILWKWKKKRPRNSYKCGTNTMERESEQTKKR 298
QY 290 ETINLKE 296
Db 299 EKIHPE 305

RESULT 13
US-08-101-624-2
; Sequence 2, Application US/08101624
; Patent No. 5942607

GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 5942607el CTLA4/CD28 Ligands and
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/101,624
FILING DATE: 26-JUL-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-101-624-2

Query Match 46.5%; Score 743.5; DB 2; Length 329;
Best Local Similarity 51.5%; Pred. No. 1.7e-60;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;
QY 1 MDPRTCTMGLAIIIFVTYLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLVFWQDQ 60
Db 1 MDPQCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPQCFANSONQSLSELVFWQDQ 60
QY 61 OKLVLYEHLGTEKLDVNAKYLGRTSFDRNNWTLRLHNQIKDMSYDCFIQKKPPTGS 120
Db 61 ENLVNEVYLGEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDGLYQCIHHKKPTGM 120
QY 121 ILQOQLTSLSVIANFSEPEIKLAQNVGTGNSGINLTCTSKQHPKPKMYFLI--TNSTN 178
Db 121 IRIHQMSLSVLANSFQPEIPIVSNITENVYINLTCSIHGYEPKPKMSVLLRTKNSI 180
QY 179 EYGNMIOSONVTELSISLSLSPDGVMHVTVCVLETSKMKISSKPLNFTQFPFS 238
Db 181 EYDGMQSQDNVTELYDVSISLSVFPDVTNSMTIFCILETDKTLRLSSPFIIEPDQ 240
QY 239 P---QTYWKEITASVTVALLLVNL--LIIVCHKPKNPQSRP-----SNTASKLERSNADR 289
Db 241 PPPDHIPW--ITAVLPVVICVWFCLILWKWKKKRPRNSYKCGTNTMERESEQTKKR 298
QY 290 ETINLKE 296
Db 299 EKIHPE 305

RESULT 14
US-08-479-744A-2
; Sequence 2, Application US/08479744A

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; Patent No. 6084067
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,744A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/280,757
; FILING DATE: 26-JUL-1994
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 28-AUG-1993
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JUL-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-479-744A-2

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Query Match 46.5%; Score 743.5; DB 3; Length 329;
Best Local Similarity 51.5%; Pred. No. 1.7e-60;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

Qy 1 MDPRTCTMGLAILIFVTLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLVFVWQDQ 60
Db 1 MDPQCTMGLSNILFWAFILSGAAPLKIQAYFNETADLPCCFANSQNSLSLVFVWQDQ 60
Qy 61 QKLVLVHYHVGTEKLDVSNAYKLGRTSFDNRNWTLLRHNVQIKDMGSDCFIQKKPPTGS 120
Db 61 ENLVLNEVYLGEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCCIHHKKPTGM 120
Qy 121 ILIQQTLTSLVIANFSEPIKLAQNVGTGNSGINLTCTSKOGHPKPKMYFLI--TNSTN 178
Db 121 IRIHQNSLSVLNFSQPEIPIVPSINTENYVINTCSSIHGYPEPKMSVLLRTKNTSI 180
Qy 179 EYGDNMQISQDNVTELFISNSLSLSPFDGVDGWHMTVVCVLETESMKISSKPLNFTQEPFS 238
Db 181 EYDGMQSQDNVTELYDVSISLSVSPFDVTNMTIFCILETDKTRLLSPFSELEDQ 240
Qy 239 P---QTYKKEITASVALLVLM--LIIVCHKKPNQFSRP----SNTASKLERDSNADR 289
Db 241 PPDPHPW--ITAVLPTVVICVMVFCLILWKWKKKRPNSYKCGTNTMERBESQTKKR 298
Qy 290 ETINLKE 296

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Db 299 EKIHIPE 305
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RESULT 15
US-08-280-757B-2
; Sequence 2, Application US/08280757B
; Patent No. 6130316
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; APPLICANT: Greenfield, Edward
; TITLE OF INVENTION: No. 6130316el CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/280,757B
; FILING DATE: 26-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JUL-1993
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-280-757B-2

Query Match 46.5%; Score 743.5; DB 4; Length 329;
Best Local Similarity 51.5%; Pred. No. 1.7e-60;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

Qy 1 MDPRTCTMGLAILIFVTLLISDAVSVEQAYFNGTAYLPCPFTKAQNISLSLVFVWQDQ 60
Db 1 MDPQCTMGLSNILFWAFILSGAAPLKIQAYFNETADLPCCFANSQNSLSLVFVWQDQ 60
Qy 61 QKLVLVHYHVGTEKLDVSNAYKLGRTSFDNRNWTLLRHNVQIKDMGSDCFIQKKPPTGS 120
Db 61 ENLVLNEVYLGEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCCIHHKKPTGM 120
Qy 121 ILIQQTLTSLVIANFSEPIKLAQNVGTGNSGINLTCTSKOGHPKPKMYFLI--TNSTN 178
Db 121 IRIHQNSLSVLNFSQPEIPIVPSINTENYVINTCSSIHGYPEPKMSVLLRTKNTSI 180
Qy 179 EYGDNMQISQDNVTELFISNSLSLSPFDGVDGWHMTVVCVLETESMKISSKPLNFTQEPFS 238
Db 181 EYDGMQSQDNVTELYDVSISLSVSPFDVTNMTIFCILETDKTRLLSPFSELEDQ 240

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Qy 239 P---QTYWKEITASVTALLVWL--LIIVCHKKPNQSRP-----SNTASKLEROSNADR 289
Db 241 PPPDHIPW--ITAVLPTVIICVMVFCLLWKKKKKKRPNYSYKCGTINIMERESEOTKKR 298
Qy 290 ETINLKE 296
Db 299 EKIHIPE 305

```

Search completed: February 13, 2003, 11:33:52
Job time : 13.1082 secs

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